

QY 241 ATCTGGTGGCCACACATCGCTCGACGCGTGTGAGAGGACTATATGCTTAAGGTGATG 300
DB 241 ATCTGGTGGCCACACATCGCTCGACGCGTGTGAGAGGACTATATGCTTAAGGTGATG 300
QY 301 CTATAGTGTATCTCTGTCGACGCGTGTGAGAGGACTATATGCTTAAGGTGATG 360
DB 301 CTATAGTGTATCTCTGTCGACGCGTGTGAGAGGACTATATGCTTAAGGTGATG 360
QY 361 TCGATTCCTCTCTCTCGACGAGTCTCTGTCCGAAGTTCCGTGTCTGTCTGTGAGAAACA 420
DB 361 TCGATTCCTCTCTCTCGACGAGTCTCTGTCCGAAGTTCCGTGTCTGTCTGTGAGAAACA 420
QY 421 AGATTGATATCCCGTATCGCTCTCTGTGAAGACGATTCGCGTTTCACTTGGTTTGAACA 480
DB 421 AGATTGATATCCCGTATCGCTCTCTGTGAAGACGATTCGCGTTTCACTTGGTTTGAACA 480
QY 481 TGACCACTGTGTAAGAAACGCTGTAACCTGTGAGATGACCAATTCGCGCCATTTAGGTTT 540
DB 481 TGACCACTGTGTAAGAAACGCTGTAACCTGTGAGATGACCAATTCGCGCCATTTAGGTTT 540
QY 541 TCATGTGCAATATTGTGCGCAAAATGGGTTACGGTGAAGTTTCAAGTGAAGTGAAGTGA 600
DB 541 TCATGTGCAATATTGTGCGCAAAATGGGTTACGGTGAAGTTTCAAGTGAAGTGAAGTGA 600
QY 601 ACATCAAGTATTTGTTTCTCTGTGAAGAGGAACTTAGCTCGGTGTTTAAAGAGCGAG 660
DB 601 ACATCAAGTATTTGTTTCTCTGTGAAGAGGAACTTAGCTCGGTGTTTAAAGAGCGAG 660
QY 661 TTAACGC 667
DB 661 TTAACGC 667

RESULT 2
AX282608
LOCUS AX282608 667 bp DNA linear PAT 02-NOV-2001
DEFINITION Sequence 6 from Patent W00177161.
ACCESSION AX282608
VERSION AX282608.1 GI:16609685
KEYWORDS
SOURCE Physcomitrella patens
ORGANISM Physcomitrella patens
REFERENCE 1
AUTHORS da Costa e Silva, O., Bohner, H.J., van Thiel, N. and Chen, R.
TITLE GTP binding stress-related proteins and methods of use in plants
JOURNAL Patent: WO 0177161-A 6 18-Oct-2001;
BASF Plant Science GmbH (DE)
FEATURES
source 1. 667
/organism="Physcomitrella patens"
/mol_type="unassigned DNA"
/db_xref="taxon:3218"

ORIGIN
Query Match 100.0%; Score 667; DB 6; Length 667;
Best Local Similarity 100.0%; Pred. No. 1,3e-193; Indels 0; Gaps 0;
Matches 667; Conservative 0; Mismatches 0;

QY 1 ATCCCGGATCCGTAGATACCAAGGCTGTGATCAATGTTCTGTAGATTGTTTACGGCT 60
DB 1 ATCCCGGATCCGTAGATACCAAGGCTGTGATCAATGTTCTGTAGATTGTTTACGGCT 60
QY 61 TTCTTGGAGATAGAGGCTGTGCGAAGAGGCCAAATCTGTTTCTGGGTCTCGACA 120
DB 61 TTCTTGGAGATAGAGGCTGTGCGAAGAGGCCAAATCTGTTTCTGGGTCTCGACA 120
QY 121 ATGCGGCAAGACTACTCTTCTGCAATGCTCAAGATGAGAACTGGGCGCAATCAAC 180
DB 121 ATGCGGCAAGACTACTCTTCTGCAATGCTCAAGATGAGAACTGGGCGCAATCAAC 180

QY 181 CAACGAGTATCCCAAGCTCAGAGAGTTGATATCAACAGATGAATTCAAAACATTCG 240
DB 181 CAACGAGTATCCCAAGCTCAGAGAGTTGATATCAACAGATGAATTCAAAACATTCG 240
QY 241 ATCTGGTGGCCACACATTCGCTCGACGCGTGTGAGAGGACTATATGCTTAAGGTGATG 300
DB 241 ATCTGGTGGCCACACATTCGCTCGACGCGTGTGAGAGGACTATATGCTTAAGGTGATG 300
QY 301 CTATAGTGTATCTCTGTCGACGCGTGTGAGAGGACTATATGCTTAAGGTGATG 360
DB 301 CTATAGTGTATCTCTGTCGACGCGTGTGAGAGGACTATATGCTTAAGGTGATG 360
QY 361 TCGATTCCTCTCTCTCGACGAGTCTCTGTCCGAAGTTCCGTGTCTGTCTGTGAGAAACA 420
DB 361 TCGATTCCTCTCTCTCGACGAGTCTCTGTCCGAAGTTCCGTGTCTGTCTGTGAGAAACA 420
QY 421 AGATTGATATCCCGTATCGCTCTCTGTGAAGACGATTCGCGTTTCACTTGGTTTGAACA 480
DB 421 AGATTGATATCCCGTATCGCTCTCTGTGAAGACGATTCGCGTTTCACTTGGTTTGAACA 480
QY 481 TGACCACTGTGTAAGAAACGCTGTAACCTGTGAGATGACCAATTCGCGCCATTTAGGTTT 540
DB 481 TGACCACTGTGTAAGAAACGCTGTAACCTGTGAGATGACCAATTCGCGCCATTTAGGTTT 540
QY 541 TCATGTGCAATATTGTGCGCAAAATGGGTTACGGTGAAGTTTCAAGTGAAGTGAAGTGA 600
DB 541 TCATGTGCAATATTGTGCGCAAAATGGGTTACGGTGAAGTTTCAAGTGAAGTGAAGTGA 600
QY 601 ACATCAAGTATTTGTTTCTCTGTGAAGAGGAACTTAGCTCGGTGTTTAAAGAGCGAG 660
DB 601 ACATCAAGTATTTGTTTCTCTGTGAAGAGGAACTTAGCTCGGTGTTTAAAGAGCGAG 660
QY 661 TTAACGC 667
DB 661 TTAACGC 667

RESULT 3
AR474304/c
LOCUS AR474304 805 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 1 from patent US 668939.
ACCESSION AR474304
VERSION AR474304.1 GI:42713152
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1
AUTHORS da Costa e Silva, O., Bohner, H.J., van Thiel, N. and Chen, R.
TITLE GTP binding stress-related proteins and methods of use in plants
JOURNAL Patent: US 668939-A 1 10-FEB-2004;
BASF Plant Science GmbH; Ludwigshafen;
MOX;
FEATURES
source 1. 805
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 98.2%; Score 655; DB 6; Length 805;
Best Local Similarity 100.0%; Pred. No. 6,4e-190; Indels 0; Gaps 0;
Matches 655; Conservative 0; Mismatches 0;

QY 5 CGGTCCTGATATACCAAGGCTGTGATCAATGTTCTGTAGATTGTTTACGGCTTCT 64
DB 781 CGGTCCTGATATACCAAGGCTGTGATCAATGTTCTGTAGATTGTTTACGGCTTCT 722
QY 65 TCGAGCATAGGCTGTGCGAAGAGGCCAAATCTGTTTCTGGGTCTCGACAATGC 124
DB 721 TCGAGCATAGGCTGTGCGAAGAGGCCAAATCTGTTTCTGGGTCTCGACAATGC 662
QY 125 TGGCAAGACTACTCTTCTGCAATGCTCAAGATGAGAACTGGGCGCAATCAAC 184
DB 125 TGGCAAGACTACTCTTCTGCAATGCTCAAGATGAGAACTGGGCGCAATCAAC 184

Db 661 TGCGAAGACTACTCTTCTGCAACATGCTCAAGATGAGAACTGGGGCAACATCAACCAAC 602
Qy 185 GCAGTATCCAAAGCTCAGAGAGATTGATATCAACAGTGAAGTTCAAGCATTTCCATCT 244
Db 601 GCAGTATCCAAAGCTCAGAGAGATTGATATCAACAGTGAAGTTCAAGCATTTCCATCT 542
Qy 245 GGGTGGCCACACAACTGCTGACGCGGTGGAGGAGCTTACTATGCTAAAGTGAATGCTAT 304
Db 541 GGGTGGCCACACAACTGCTGACGCGGTGGAGGAGCTTACTATGCTAAAGTGAATGCTAT 482
Qy 305 AGTGTATCTGCTGACGCACTGACAGAGAGATTGCTGAGTCAAAAGAAAGCTCGA 364
Db 481 AGTGTATCTGCTGACGCACTGACAGAGAGATTGCTGAGTCAAAAGAAAGCTCGA 422
Qy 365 TTCTCTTCTCTCGACGATTTCTGTGTCCCAAGTTCCGTGCTGCTGCTGGGAAACAAGAT 424
Db 421 TTCTCTTCTCTCGACGATTTCTGTGTCCCAAGTTCCGTGCTGCTGCTGGGAAACAAGAT 362
Qy 425 TGAATATCCGTAAGCTTCTCTGAAAGAGATTGCGGTGACACTTGGGTTGACATGAC 484
Db 361 TGAATATCCGTAAGCTTCTCTGAAAGAGATTGCGGTGACACTTGGGTTGACATGAC 302
Qy 485 CACTGTAAAGAAAGCGGTGAACCTGGGAGATAGCAACATTCGGCCATTGAGGTTTTCAT 544
Db 301 CACTGTAAAGAAAGCGGTGAACCTGGGAGATAGCAACATTCGGCCATTGAGGTTTTCAT 242
Qy 545 GTGCAATATTGTGGCGAAATGGGGTACGCTGAAGTTTCAAGTGAATGACCCAGTACAT 604
Db 241 GTGCAATATTGTGGCGAAATGGGGTACGCTGAAGTTTCAAGTGAATGACCCAGTACAT 182
Qy 605 CAAGTATTGTTTCTCTGTGAAGAGAACTTAGCTGGGTGTTAAGAGGACGA 659
Db 181 CAAGTATTGTTTCTCTGTGAAGAGAACTTAGCTGGGTGTTAAGAGGACGA 127

RESULT 4
AX282603/c 805 bp DNA linear PAT 02-NOV-2001
LOCUS AX282603
DEFINITION Sequence 1 from Patent WO0177161.
ACCESSION AX282603
VERSION AX282603.1 GI:16609680
KEYWORDS
SOURCE
ORGANISM
Phycomitrella patens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariaceae; Funariaceae; Funariaceae; Phycomitrella.

REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
SOURCE
1. 805
/organism="Phycomitrella patens"
/mol_type="unassigned DNA"
/db_xref="taxon:3218"

ORIGIN
Query Match 98.2%; Score 655; DB 6; Length 805;
Best Local Similarity 100.0%; Pred. No. 6,4e-190; Indels 0; Gaps 0;
Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CGGGTCCGTAGATACCAAGGCTGTGACCATGTTTCTGTAGATTGTTTTCAGGCTTTCT 64
Db 781 CGGGTCCGTAGATACCAAGGCTGTGACCATGTTTCTGTAGATTGTTTTCAGGCTTTCT 722
Qy 65 TGGCAGCATAGAGGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 124
Db 721 TGGCAGCATAGAGGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 662
Qy 125 TGGCAAGACTACTCTTCTGACATGCTCAAGATGAGAACTGGGGCAACATCAACCAAC 184
Db 661 TGGCAAGACTACTCTTCTGACATGCTCAAGATGAGAACTGGGGCAACATCAACCAAC 602

Qy 185 GCAGTATCCAAAGCTCAGAGAGATTGATATCAACAGTGAAGTTCAAGCATTTCCATCT 244
Db 601 GCAGTATCCAAAGCTCAGAGAGATTGATATCAACAGTGAAGTTCAAGCATTTCCATCT 542
Qy 245 GGGTGGCCACACAACTGCTGACGCGGTGGAGGAGCTTACTATGCTAAAGTGAATGCTAT 304
Db 541 GGGTGGCCACACAACTGCTGACGCGGTGGAGGAGCTTACTATGCTAAAGTGAATGCTAT 482
Qy 305 AGTGTATCTGCTGACGCACTGACAGAGAGATTGCTGAGTCAAAAGAAAGCTCGA 364
Db 481 AGTGTATCTGCTGACGCACTGACAGAGAGATTGCTGAGTCAAAAGAAAGCTCGA 422
Qy 365 TTCTCTTCTCTCGACGATTTCTGTGTCCCAAGTTCCGTGCTGCTGCTGGGAAACAAGAT 424
Db 421 TTCTCTTCTCTCGACGATTTCTGTGTCCCAAGTTCCGTGCTGCTGCTGGGAAACAAGAT 362
Qy 425 TGAATATCCGTAAGCTTCTCTGAAAGAGATTGCGGTGACACTTGGGTTGACATGAC 484
Db 361 TGAATATCCGTAAGCTTCTCTGAAAGAGATTGCGGTGACACTTGGGTTGACATGAC 302
Qy 485 CACTGTAAAGAAAGCGGTGAACCTGGGAGATAGCAACATTCGGCCATTGAGGTTTTCAT 544
Db 301 CACTGTAAAGAAAGCGGTGAACCTGGGAGATAGCAACATTCGGCCATTGAGGTTTTCAT 242
Qy 545 GTGCAATATTGTGGCGAAATGGGGTACGCTGAAGTTTCAAGTGAATGACCCAGTACAT 604
Db 241 GTGCAATATTGTGGCGAAATGGGGTACGCTGAAGTTTCAAGTGAATGACCCAGTACAT 182
Qy 605 CAAGTATTGTTTCTCTGTGAAGAGAACTTAGCTGGGTGTTAAGAGGACGA 659
Db 181 CAAGTATTGTTTCTCTGTGAAGAGAACTTAGCTGGGTGTTAAGAGGACGA 127

RESULT 5
AX721083 928 bp mRNA linear PAT 07-MAY-2003
LOCUS AX721083
DEFINITION Sequence 43 from Patent WO0220754.
ACCESSION AX721083
VERSION AX721083.1 GI:30421919
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
SOURCE
1. 928
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/note="Incyte ID No: LI:722913.1:2000SEP08"

ORIGIN
Query Match 51.0%; Score 340.4; DB 6; Length 928;
Best Local Similarity 74.7%; Pred. No. 4.5e-93;
Matches 441; Conservative 0; Mismatches 146; Indels 3; Gaps 1;

Qy 23 GCGTGTACAGATTTCTTGTAGATTGCTTTCAGGCTTTCTGCGAGCATAGGGGCTG 82
Db 153 GGTGGGGAGATGTTCTCTGGAATGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 212
Qy 83 GCAGAAAGAGCCAAATCTGTTTCTGAGTCTGCAATGCTGCAAGACTACTCTTCT 142

Db 213 GCAAGAGAGCCCAAGATCTCTCTTGGCTCGACACGCCGCGCAAGACCAAGCTGCT 272

Qy 143 GCACATGCTCAAGAGATGAGAAATCGGGCAACATCAACCAACGAGATATCCAGCTGAGA 202

Db 273 CCACATGCTCAAGAGACGAGCGGTGTGTCACACACGACGACGACGCCGACGCTCGGA 332

Qy 203 GGAATTGATTCACACAGAGTGAAGTTCAAAGCATTCGATCTGGGTGGCCACACATTCGC 262

Db 333 GGACCTCGACATCGGCAAGATCAAGTTCMAAGCCGTTCACTCGCGGCCCAAGATTCGC 392

Qy 263 TCGACGCGTGTGAGAGGAGCTACTATAGTAAGTGATGATGATCTCTGTCGACGC 322

Db 393 GCGCGCGCTGTGAGAGATTACTACGCAAGCTGATGCTAGTATACCTGATGATGC 452

Qy 323 AGTAGACAGGAGAGATTTGTGAGTCAAGAAAGAGCTCGATTCCTTCTTCGACGA 382

Db 453 ATATGATTAAGAGGAGATTTGCTGATCAAAAGAGAGCTGCTCTCTGCTGATGA 512

Qy 383 TTCTCTGTCCTCAAGTTCCTGCTGCTGCTGCTGGAACCAAGTTCATCCGTAACGCTTC 442

Db 513 TTCTTTGGCCCAATGTTCAATTTCTCATCTTGGCAACAGATGATATCCATATGCTGC 572

Qy 443 TTCTGAGACAGAGTTCGGCTTCAACACTTGGGTGACCA--TGAACCTGGTAAAGGAC 499

Db 573 CTCTGAAGAGAGCTACCGTATACACTAGCCCTTAGCACTTCACAAACGGAGAGGCA 632

Qy 500 GGTGAACCTGGAGATAGCAACATTCGCGCCCATGAGGTTTTCATGTGCACTATTTGTCG 559

Db 633 GGTCAACCTTGGCGCACTCCATGTCGTCGCACTTGAAGGTTCTTCATGTGCACTGTTGTTGC 692

Qy 560 CAAATGGGGTATCGGTGAAGTTTTCAGTGAATGACCAAGTACATCAAGT 609

Db 693 CAAGATGGGCTACGCTGATGATGTTTCMAAGTGGGCTCTCCAGTACATCAAGT 742

RESULT 6

AK099125

LOCUS ORYZA sativa (japonica cultivar-group) cDNA clone:J023044P12, full insert sequence.

DEFINITION AK099125 927 bp mRNA linear PLN 24-JUL-2003

ACCESSION AK099125

VERSION AK099125.1 GI:32984334

KEYWORDS FULL_CDNA; CAP trapper.

SOURCE ORYZA sativa (japonica cultivar-group)

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1

AUTHORS The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team; Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotte,I., Ohtsuki,K., Shimizu,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group; Ohtomo,Y., Murakami,K., Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y., Kuroseki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M., Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Nishikawa,J., Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Mura,J., Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN; Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Hayatsu,N., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Ohtsuki,N., Oka,Y., Saito,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Yoshino,M., and Hayashizaki,Y.

TITLE Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice

JOURNAL Science 301 (5631), 376-379 (2003)

REFERENCE PUBMED 12869764

AUTHORS 2 (bases 1 to 927)

Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K., Fujimura,T., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W.,

Hayashida,K., Hayashizaki,Y., Hayatsu,N., Hiramoto,K., Hirooka,T., Horii,F., Hotte,I., Iida,J., Iida,Y., Ikeda,R., Imamura,K., Imotani,K., Ishibiki,J., Ishii,Y., Ishikawa,M., Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawagashira,N., Kawai,J., Kawamata,M., Kikuchi,S., Kishikawa-Hirozane,T., Kishimoto,N., Kobayashi,M., Kodama,T., Kojima,K., Kojima,Y., Kondo,S., Konno,H., Koude,M., Koya,S., Kurihara,C., Kuroseki,T., Kusumegi,T., Li,C., Lu,M., Masuda,H., Matsubara,K., Matsuyama,T., Mura,J., Miyazaki,A., Mizuno,K., Murakami,K., Murata,M., Nagata,T., Nakamura,M., Namiki,T., Narikawa,R., Nikura,J., Nishi,K., Nomura,K., Numasaki,R., Ohneda,E., Ohno,M., Ohtsuki,K., Oka,M., Ooka,H., Ohtsuki,N., Oka,Y., Ohtsuki,Y., Ryu,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Satoh,K., Shibata,K., Shinagawa,A., Shiraki,T., Shishiki,T., Sogabe,Y., Sugano,S., Sugiyama,A., Suzuki,K., Suzuki,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Takeku-Akashira,S., Tanaka,T., Tomaru,A., Toya,T., Tsunoda,Y., Ueda,M., Waki,K., Xie,Q., Yahagi,W., Yamada,H., Yamamoto,M., Yasunishi,A., Yazaki,J., Yokomizo,S., and Yoshimura,A.

Direct Submission

Submitted (27-AUG-2002) Shoeni Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kamondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:kikuchi@nias.affrc.go.jp, tel:81-29-858-7007, fax:81-29-858-7007)

This clone is one of the 28k full-length cDNA clones from japonica rice.

URL: //cdna01.dna.affrc.go.jp/cdna/

NIAS Rice Full-length cDNA Project Team: Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotte,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T., and Yamamoto,M.

FAIS Genome Sequencing & Analysis Group: Ohtomo,Y., Iida,Y., Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M., Kodama,T., Kuroseki,T., Kusumegi,T., Lu,M., Masuda,H., Mura,J., Mizuno,K., Narikawa,R., Nikura,J., Oka,M., Ryu,R., Sugano,S., Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S., Yoshimura,A., Matsubara,K., and Murakami,K.

Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hirooka,T., Horii,F., Iida,J., Imamura,K., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawai,J., Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Konno,H., Koude,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Ohtsuki,N., Oka,Y., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Takeku-Akashira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K., Yasunishi,A., and Hayashizaki,Y.

LOCATION/Qualifiers

1..927

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nipponbare"

/db_xref="taxon:39947"

/clone="J023044P12"

FEATURES

source

ORIGIN

Query Match 49.5%; Score 330.4; DB 15; Length 927;

Best Local Similarity 74.3%; Prod. No. 5.3e-90;

Matches 431; Conservative 0; Mismatches 146; Indels 3; Gaps 1;

Qy 33 ATGTTCTTGTAGATTGTTTACGCGCTTCTTGCAGCATTAAGGCTGTGGCAAGAGAG 92

Db 127 ATGTTCTGCTGAGCTGCTTCTTACGCGGCTGCTGCGCTGCGGCTGTGTGCAAGAGAG 186

Qy 93 GCCAAAATCTGTTGCTGCGCTTCGACCAAGCTCGGCAAGACTCTCTTCGCAACAGCTC 152

Db 187 GCGAAGATCTCTTCTCGGCTCGACCAAGCGCGCAAGACGAGCTCTCCACATGCTC 246

OY	153	AAGATGAGAACTGGGGCAATCAACCAACGAGTATCAAGTACAGAGATTGAT	212
Db	247	AAGACGAGAAATTGGTGCAGATCAACTACGCAATACCGACTTTGAAGAGCTGAC	306
OY	213	ATCAACAGAGTGAAGTTCAAGCAATTCGATCGGTGGCCAACAATCGCTCGACGCTG	272
Db	307	ATTGGGAAGATCAAGTTCAAGCGCTTTGATTTAGGAGGCCATCAAAATTGCTCGCCGTGTG	366
OY	273	TGGAGGAGCTACTATNGCTAAAGTGGATTCCTATAGTATTCCTCGACAGTATGACAG	332
Db	367	TGGAAGACTACTATNGCTAAAGTGGATTCCTATAGTATTCCTCGACAGTATGACAG	426
OY	333	GAGAGATTGCTGAGTCAAGAAAGCTGATTTCTTTCTCTCGACGATTTCTGTGCC	392
Db	427	GAGAGATTCTCGAGTCAAGAAAGCTGATTTCTTTCTCTCGACGATTTCTGTGCC	486
OY	393	CAAGTCTCTGTGCTGCTCTGGGAAACAAGTATGATATCCGCTACGCTTTCTTGGAAAC	452
Db	487	ACCGTCCCTTCTGATCTTGGGCAACAAGATCGATCCCTACGCGCGCTCGAGGAG	546
OY	453	GAGTTGCGGTTCAACCTTGGGTTGACCA---TGACCACTGGTAAAGAACGATGAACCTG	509
Db	547	GAGCTCGGCTACACATGAGGGGTAGCAACTTCAACACCGGCAAGGGGATGAGCCTC	606
OY	510	GGAGATAGCAACATTCGGCCCATTTGAGGTTTTCATGTCAAGTATTTGTGCGAAATGGGG	569
Db	607	GGCGAGTCCAAAGTTCCGCCCCCTGGAGGTGTTCATGTCAAGCAATTCGTCCGCAAGATGGGC	666
OY	570	TACGGTGAAGGTTTCAAGTGAATGACCCAGTACATCAAGT	609
Db	667	TATGGGATGGGTTCAAGTGGGTGTCAACGATACATCAAGT	706

Horii, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K., Imoto, K., Ishibori, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanegawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Maesuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M., Namiki, T., Narikawa, R., Nikura, J., Niishi, K., Nomura, K., Numasaki, R., Ohneda, E., Omo, W., Ohtsuki, K., Oka, M., Ooka, H., Otsu, N., Ota, Y., Otsu, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shinozawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toyota, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yanagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yoshimura, A.

Direct Submission

Submitted (05-DEC-2001) Shoichi Kikuchi, National Institute of Agricultural Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression, 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:ekikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7008)

This clone is one of the 28K full-length cDNA clones from japonica rice.

URL: http://cdna01.dna.affrc.go.jp/cDNA/NIAS_Rice_Full-length_cDNA_Project_team:kikuchi.S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yanagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T. and Yamamoto, M.

Partial Sequence Sequencing & Analysis: Genom: Otsu Y Iida Y

LOCUS	AK060332	552 bp	mRNA	linear
DEFINITION	Oryza sativa (japonica cultivar-group) cDNA clone:001-008-B07, full-length sequence.			
ACCESSION	AK060332			
VERSION	AK060332.1	GI:32970350		
KEYWORDS	FLI cDNA; oligo-capping.			
SOURCE	Oryza sativa (japonica cultivar-group)			
ORGANISM	Oryza sativa (japonica cultivar-group)			
REFERENCE	Enkayotca Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoidae; Oryzace; Oryza.			
REFERENCE	1			
AUTHORS	The Rice Full-length cDNA Consortium, National Institute of Agricultural Sciences Rice Full-length cDNA Project Team; Kikuchi,S., Satoh,K., Nagata,T., Kawagashita,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Nemiki,T., Ohneda,E., Yahagi,M., Suzuki,K., Li,C., Ohtsuki,K., Shibiki,T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group; Otsomo,Y., Murakami,K., Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y., Kuratsaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M., Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Nikiura,Y., Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Miura,J., Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN; Kawaji,J., Carninci,P., Adachi,J., Aizawa,K., Aizawa,T., Fukuda,S., Hara,A., Hashidume,W., Hayatsu,N., Imotani,A., Ishii,Y., Itoh,M., Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Osato,N., Ota,Y., Saito,R., Saeki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Yoshino,M. and Hayashizaki,Y.			
TITLE	Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice			
JOURNAL	Science 301 (5631), 376-379 (2003)			
PUBMED	12869764			
REFERENCE	2 (bases 1 to 952)			
AUTHORS	Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K., Fujimura,T., Fukuda,S., Hanagaki,T., Hara,A., Hashidume,W., Hayashida,K., Hayashizaki,Y., Hayatsu,N., Hiramoto,K., Hirata,K., Hayashida,K., Hayashizaki,Y., Hayatsu,N., Hiramoto,K., Hirata,K.,			

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Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S.,
Yoshimura,A., Matsubara,K. and Murakami,K.
Genome Exploration Research Group in Riken Genomic Sciences Center
and Genome Science Laboratory in Riken Adachi,J., Aizawa,K.,
Aikawa,T., Arikawa,T., Carninci,P., Fukuda,S., Hangaki,T.,
Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K.,
Hiraoka,T., Horii,F., Iida,Y., Imamura,K., Imocani,K., Ishii,Y.,
Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawaji,J.,
Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,I., Murata,M.,
Nakamura,M., Nishii,K., Nomura,K., Numasaki,R., Ohno,M., Osato,N.,
Ota,Y., Satoh,H., Sakai,C., Sakai,K., Sakazune,N., Sano,H.,
Sasaki,D., Sato,K., Shibata,K., Shingawa,A., Shiraki,T.,
Sogabe,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F.,
Takahashi,A., Tanaka,T., Tomaru,A., Toyota,T., Waki,K.,
Yasunishi,A. and Hayashizaki,Y.
Location/Qualifiers
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 DB 310 ATTGGGAGAGTCAAGTTCMAAGCCTTTGATTTAGAGAGCCATCAAAATGCTCGCCGTG 369
 QY 273 TGGAGGAGCTACTATGCTAAGTGGATGCTATAGTGTATCTCGTGAACGAGTGAAG 332
 DB 370 TGGAAAGACTACTATGCTAAGTGCAGCGGGTGTCTACCTCGTGAATGCTAGACAAG 429
 QY 333 GAGGATTTGCTGATCAAAAGAGCTGATCTCTCTCTCCGACGATCTCTCTCC 392
 DB 430 GAGAGGTTCTCGAGTGAAGAAAGAGCTGACCGCTCTCTCTGAGACACTCTCTGACC 489
 QY 393 CAAGTTCCTGTGCTGCTCTGGGAAAAGAGTATATCCGATGAGCTTCTTCTGAAAGAC 452
 DB 490 ACCGTCCCTCTCTGATCTCTGGCAACAGTGCACATCCCTACGCGCGCTCGAGAGAG 549
 QY 453 GAGTTGCGGTTACACTTGGGTTGACCA--TGACCACTGGTAAAGAACCGTGAACCTG 509
 DB 550 GAGCTCCGCTACCACTGGGCTGAGCAACTTACCAACCGGCAAGGAGGTTGAGCTC 609
 QY 510 GGAATAGCAACATTCGCGCCATTGAGGTTTCAATGTCAGTATTTGGCCCAAAATGGGG 569
 DB 610 GGCAGTTCACAGTTCGCGCCCTGAGAGTGTTCATGTGACAGCATGTCGCCAAGATGGC 669
 QY 570 TACGGTGAAGGTTCAAGTGAATGACCCAGTACATCAAGT 609
 DB 670 TATGGGATGGGTTCAAGTGGGTGTCACTACATCAAGT 709

RESULT 8
 AY596178 945 bp mRNA linear PLN 08-MAY-2004
 LOCUS
 Zea mays putative ras-like small GTP binding protein mRNA, complete cds.
 ACCESSION
 AY596178.1 GI:46946655
 VERSION
 AY596178.1 GI:46946655
 KEYWORDS
 Zea mays
 ORGANISM
 Zea mays
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.

REFERENCE
 AUTHORS
 TITLE
 Zea mays
 Suppressing apoptosis is a key mechanism of maize S-CMS restore gene R13
 Unpublished
 2 (bases 1 to 945)
 Zhang, Z., Tang, W. and Zheng, Y.
 Direct Submission
 Submitted (11-APR-2004) National Key Lab of Crop Genetic Improvement, Huangzhong Agricultural University, Wuhan, Hubei 430070, China

FEATURES
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ORIGIN

Query Match 49.4%, Score 329.2, DB 15, Length 945;
 Best Local Similarity 73.1%, Pred. No. 1, 2e-89;
 Matches 437; Conservative 0; Mismatches 158; Indels 3; Gaps 1;

QY 19 CCAAGGCTGTCACCAAGTTCTTGTAGATTGTTTAACGGCTTCTTGGAGATAGGGC 78
 DB 57 CCGAGATTGAAAGATGTTCTGTGACTGAGTCTTATGAGGAGTGGACATCGCTTGGC 116
 QY 79 TGTGCAAGAGAGGAGCCAAATCTGTTTCTGGGCTCGCAATGCTGGCAAGTACTC 138
 DB 117 TGTGCAAGAGAGGAGTATGATCTCTTCTTGGCTCGCAACGCGGGAACACACCC 176
 QY 139 TTGTGCAATGCTCAAGATGAGAACTGGGCAACATCAACCAAGCATATCAAGT 198
 DB 177 TCTTCAATGCTGAAGAGAGAGCGGCTGTACAGACCAAGCAGCAGCATGCCACGT 236
 QY 199 CAGAGAGTTGATATCAACAGATGAAGTCAAAACATTCGATCGGGTGGCACACA 258
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 DB 297 TCGCGCGCGCGCTGTGAGAGACTACTAGCCAGGTTGATGCTGTGTGTA 356
 QY 319 ACCAGTGAACAGAGAGAGATTGCTGAGTCAAAAGAAAGCTGATCTTCTCTCCG 378
 DB 357 ATGCTGTGCAAGAGAACTTTTCCGAGTCGAAGAGGAGCTTGAATGCGCTTCTGAC 416
 QY 379 AGCATCTCTGTCGCCAAGTTCTGTGCTGCTCTCGGAAAACAAGTTGATATCCGATG 438
 DB 417 ATACTCTCTTGAACGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 476
 QY 439 CTCTCTCTGAAGAGAGTTCGCTGCTCACTTGGTTCACCA--TGACCACTGTGTAAG 495
 DB 477 CGGCTTGAAGAGAGAGCTGAGTACTACTCGGCTGAGCACTTACACACGGGGAAG 536
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 DB 537 GCAACGTGAACCTGGCGGCACTCCAAATGTCGCGCCCTGGAAGATCTTATGTGAGTGTG 596
 QY 556 TGGCAAAATGGGGTACGGTGAAGTTTCAAGTGAATGACCCAGTACATCAAGTATG 613
 DB 597 TGGCAAGATGGGCTATGGGAAAGGCTTCAATGAGATGTCTCACTACATCAAGTATG 654

RESULT 9
 AK099149 934 bp mRNA linear PLN 24-JUL-2003
 LOCUS
 Oryza sativa (japonica cultivar-group) cdna clone:J023063C05, full insert sequence.
 DEFINITION
 AK099149
 AK099149.1 GI:32984358
 ACCESSION
 AK099149.1 GI:32984358
 VERSION
 AK099149.1 GI:32984358
 KEYWORDS
 FLI CDNA; CAP trapper.
 SOURCE
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 ORGANISM
 Eubharitoidae; Oryzaceae; Oryza.

REFERENCE
 AUTHORS
 The Rice Full-length cDNA Consortium, National Institute of Agricultural Sciences Rice Full-length cDNA Project Team,
 Kikuchi, S., Satoh, K., Nagata, T., Kawasashira, N., Doi, K.,
 Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotra, I.,
 Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C.,
 Ohtsuki, K., Shienki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group, Otsu, Y., Murakami, K.,
 Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsumoda, Y.,
 Kurotaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M.,
 Nariwaka, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Nikiura, J.,
 Ikeda, R., Ishiki, J., Kawamata, M., Yoshimura, A., Mura, J.,
 Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN,
 Kawai, J., Carninci, P., Adachi, T., Aizawa, K., Aizawa, T., Fukuda, S.,

TITLE Hara, A., Hashidume, W., Hayatsu, N., Imolani, K., Ishii, Y., Itoh, M., Kaga, I., Kondo, S., Kono, H., Miyazaki, A., Oasato, N., Ota, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shingawa, A., Shiraki, T., Yoshino, M., and Hayashizaki, T.
Journal Collection, mapping, and annotation of over 28,000 cDNA clones from Japanese rice
Journal Science 301 (5631), 376-379 (2003)

REFERENCE
AUTHORS

2 (Pages 1 to 934)

Adachi, Y., Aizawa, K., Akimura, T., Arikawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanaegaki, T., Hara, A., Hehizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T., Horii, F., Hotta, I., Iida, Y., Iida, Y., Ikeda, R., Imamura, K., Imotani, K., Iribiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murakami, M., Nagata, T., Nakamura, M., Namiki, T., Nariikawa, R., Nilkura, Y., Nishi, K., Nomura, K., Numaeki, R., Ohneda, E., Ohno, M., Ohnuki, K., Oka, M., Ooka, H., Oeato, N., Ota, Y., Otomo, Y., Ryu, R., Satoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shikagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takuu-Khahira, S., Tanaka, T., Tomaru, A., Toyo, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yoshimura, A.

COMMENT

TITLE
JOURNAL

URL: <http://cdnaat.dna.affrc.go.jp/cDNA/NRAS Rice Full-length cDNA Project Team>: Kikuchi, S., Satoh, K., Negata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, I., Kojima, K., Naituki, T., Onhed, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuka, K., Shienkhi, T. and Yamamoto, M.

FAIS Genome Sequencing & Analysis Group: Ootomo, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishihiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurotaki, T., Kusumegi, T., Lu, M., Masuda, H., Murata, J., Mizuno, K., Naitkawa, R., Nikiura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, C. and Murakami, K.

Genome Exploration Research Group in Riken: Adachi, J., Aizawa, K., Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Atimura, T., Arakawa, T., Carrilho, P., Fukuda, S., Hanagaki, T., Harata, H., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N., Ota, Y., Satoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takachi-Akahira, S., Tanaka, T., Tomaru, A., Toyota, T., Waki, K., Yaenishi, A. and Hayashizaki, Y.

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FEATURES
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ORIGIN

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Matches 430	Conservative	0	Mismatches 147	Indels 3
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Qy	33	ATGTTCTGTGATAGATGGCTTTTACGGCTTTCTTCGAGCAATAGGGCTGTGAGCAAGAG	92
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Qy	93	GCCAAATTCCTGTTTCTGGGTCTGCACAATCTGGCAAGACTACTCTTCTGCAATGCTC	152
Db	190	GCCAAGATCTCTTCTCGGCTCGACAAACCCCGCAAGACACACGCTCTTCCACATGCTC	249
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Qy	453	GAGTTCGGTTTCACTTGGGTTGACA---TGAACAATGTGTAAAGGAACGTGAACCTG	509
Db	550	GAGCTCCGTTACCAATGGGGCTGACGAATTTCAACAACCGGCAAGGCAAGGTGAGCTTC	609
Qy	510	GGAGATGACAATTCGGGCCATTGAGGTTTTCATGTGCAATATTGTGCGCAAAATTTGGG	569
Db	610	GGGAGTCCAAAGTTTCGCCCCCTGGAGGTGTTTCATGTGCAGACATCTGTCCGCAAGATGGGC	669
Qy	570	TACGTGAAGTTTCAATGATGACGACCAAGTACATCAAGT	609
Db	670	TATGGGATGGGTTCAAGTGGGTGCACGATCACTCAAGT	709

RESULT 10	AK112012	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE
	AK112012	1094 bp	mRNA						
	Oryza sativa (japonica cultivar-group)		linear						PLN 29-OCT-2003
	insert sequence.		cdna clone:006-210-H07, full						
	AK112012								
	FLI CDNA: oligo capping.								
	AK112012.1	GI:37986875							
	Oryza sativa (japonica cultivar-group)								
	Oryza sativa (japonica cultivar-group)								
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;								
	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;								
	Eleusineaceae; Oryzaceae; Oryza.								

REFERENCE
AUTHORS

1. The Rice Full-length cDNA Consortium, National Institute of Agricultural Sciences Rice Full-length cDNA Project Team, Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yasaki, T., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group, Otonari, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Naitaka, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Mikiura, J., Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Nakra, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matubara, K., RIKEN, Kawai, J., Carninci, P., Adachi, N., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashidate, W., Hayatsu, N., Imotani, K., Iselli, Y., Itoh, M.,

TITLE	Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Otsu, N., Ota, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M. and Hayashizaki, Y.		
	Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice		
JOURNAL	Science	301 (5611)	376-379 (2003)
PUBMED	12869764		
REFERENCE	2		
	Aachai, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hizemoto, K., Hirooka, T., Hori, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K., Imotani, K., Ieshibiki, J., Ieshi, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Konda, M., Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Murekami, K., Murata, M., Nagata, T., Nakahama, Y., Nakamura, M., Namiki, T., Narikawa, R., Nikura, J., Nishii, K., Nomura, K., Numasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H., Otsu, N., Ota, Y., Otsu, Y., Otsu, M., Otsu, K., Otsu, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shinagawa, A., Shiraki, T., Shihiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaki-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yoshimura, A.		
TITLE	Rice full-length cDNA		
JOURNAL	Unpublished		
REFERENCE	3 (bases 1 to 1094)		
AUTHORS	Kikuchi, S.		
TITLE	Direct Submission		
JOURNAL	Submitted (12-SRP-2002) Shoshi Kikuchi, National Institute of Agricultural Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression, 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)		
COMMENT	This clone is one of the 32k full-length cDNA clones from japonica rice.		
	URL: http://cdna01.dna.affrc.go.jp/cDNA/NIAS_Rice_Full-length_cDNA_Project_Team_Kikuchi_S_Satoh_K_Nagata_T_Kawagashira_N_Doi_K_Kishimoto_N_Yazaki_J_Ishikawa_M_Yamada_H_Ooka_H_Hotta_I_Kojima_K_Namiki_T_Ohneda_E_Yahagi_W_Suzuki_K_Li_C_Ohtsuki_K_Shishiki_T_Yamamoto_M_and_Nakahama_Y		
FEATURES	PLS Genome Sequencing & Analysis Group: Otsu, Y., Iida, Y., Fujimura, T., Ikeda, R., Ieshibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kuroseki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Narikawa, R., Nikura, J., Oka, M., Ryo, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K. and Murakami, K.		
	Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hizemoto, K., Hirooka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ieshi, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Konda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishii, K., Nomura, K., Numasaki, R., Otsu, N., Ota, Y., Satoh, K., Sasaki, D., Sato, K., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaki-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A. and Hayashizaki, Y.		
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	The Rice Full-length cDNA Consortium, National Institute of Agricultural Sciences Rice Full-length cDNA Project Team, Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohtsuki, K., Shishiki, T., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International		

Science Genome Sequencing & Analysis Group: Otomo, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Nikura, J., Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Mura, J., Kusunegi, T., Oka, M., Ryu, R., Ueda, M., Matubara, K., RIKEN: Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kondo, S., Kono, H., Miyazaki, A., Otsu, N., Ota, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M., and Hayashizaki, Y.

TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice
Science 301 (5631), 376-379 (2003)
12869764

2 (bases 1 to 1152)
Adachi, U., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hirooka, T., Hori, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kurihara, C., Kurosaki, T., Kusunegi, T., Li, C., Lu, M., Masuda, H., Matubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M., Namiki, T., Narikawa, R., Nikura, J., Nishi, K., Nomura, K., Numaaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H., Otsu, N., Ota, Y., Otomo, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shiragami, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahita, S., Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S., and Yoshimura, A.

TITLE
JOURNAL
COMMENT
Submitted Submission
Direct Submission
Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of Agricultural Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kamondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail: kikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 28k full-length cDNA clones from japonica rice.
URL: http://cdna01.dna.affrc.go.jp/cDNA/NIAS_Rice_Full-length_cDNA_Project_Team_Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and Yamamoto,M.

FAIS Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusunegi, T., Lu, M., Masuda, H., Mura, J., Mizuno, K., Narikawa, R., Nikura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K., and Murakami, K.
Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numaaki, R., Ohno, M., Otsu, N., Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahita, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A., and Hayashizaki, Y.

FEATURES
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location/Qualifiers

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Matches 440; Conservative 0; Mismatches 168; Indels 3; Gaps 1;

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QY 481 --TGACCACTGTGAAGAGAGCTGACCTGAGGAGATGCAACATTCGCGCCCATTTAGGT 538
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LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone:001-008-G03, full insert sequence.
ACCESSION
AK111979
VERSION
AK111979.1 GI:37988642
KEYWORDS
F11_CDNA; oligo capping.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; Eriactroideae; Oryzoideae; Oryza.
REFERENCE
AUTHORS
1 The Rice Full-length cDNA Consortium, National Institute of Agricultural Sciences Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K.,

protein (GBP) mRNA, complete cds.
 AY620417
 VERSION GI:47499877
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 ORGANISM
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 REFERENCE
 1 (bases 1 to 1086)
 Meng, X.-B., Lin, R.-M., Wang, M., Zhao, W.-S. and Peng, Y.-L.
 Molecular cloning and expression of a Magnaporthe grisea induced
 cDNA encoding a small GTP-binding protein
 Unpublished
 2 (bases 1 to 1086)
 Meng, X.-B., Lin, R.-M., Wang, M., Zhao, W.-S. and Peng, Y.-L.
 Direct Submision
 Submitted (21-APR-2004) Plant Pathology, China Agricultural
 University, West Road No. 2 of Yuanmingyuan Haidian, Beijing,
 Beijing 100094, China
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 ORIGIN
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 Matches 429; Conservative 0; Mismatches 150; Indels 3; Gaps 1;
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QY 453 GAGTGGGTTCACTTGGGTTGACCA---TGACCACTGGTAAAGAAAGGTAACCTG 509
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model1

Run on: December 8, 2005, 21:11:50 ; Search time 476 Seconds
(without alignments)
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues
Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: geneseqn2001as:*
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14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	335.6	50.3	955	13	ADK46899
8	332.4	49.8	966	13	ADK30716
9	332.4	49.8	1017	13	ADK62537
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11	331.2	49.7	830	11	ADM45760
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22	318.8	47.8	928	13	ADK29066	AdK29066 Plant full
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24	313	46.9	807	13	ADR60521	AdR60521 Cotton CD
25	312.8	46.9	994	13	ADR60522	AdR60522 Cotton CD
26	312.6	46.9	885	3	AAK42538	AAK42538 Arabidops
27	312.6	46.9	1047	13	ADR60523	AdR60523 Cotton CD
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29	310	46.5	689	11	ADM45514	Adm45514 Insect re
30	310	46.5	689	11	ADM45782	Adm45782 Insect re
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34	295	44.2	675	6	ABO65802	ABO65802 Arabidops
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38	292	43.8	582	3	AAK42867	AAK42867 Arabidops
39	272.6	40.9	569	13	ACN48893	ACN48893 Cotton pr
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43	266.6	40.0	580	11	ADM45500	Adm45500 Insect re
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ALIGNMENTS

RESULT 1
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XX ABN89814;
DT 18-SEP-2002 (first entry)

DE Physcomitrella patens GBP-1 encoding cDNA sequence SEQ ID NO:6.

XX Physcomitrella patens; GBP; GTP binding protein; GBSRP; plant;
XX GTP binding stress-related protein; transgenic plant; agricultural;
XX environmental stress; salinity; drought; temperature; gene; ss.

XX Physcomitrella patens.

XX Key Location/Qualifiers

FT CDS 33..611

FT /tag= a /product= "GTP-binding protein 1 (GBP-1)"

XX US2002066124-A1.

XX 30-MAY-2002.

XX 06-APR-2001, 2001US-00828310.

XX 07-APR-2000; 2000US-0196001P.

XX (SILV/) SILVA O D C E.

XX (BOHN/) BOHNERT H J.

XX (THIE/) THIELEN N V.

XX (CHEN/) CHEN R.

XX Silva ODCE, Bohnert HJ, Thiele N, Chen R;

XX WPI: 2002-556781/59.

XX P-PDB; ABB81583.

XX Novel GTP binding stress-related proteins and genes encoding the

XX proteins, useful for producing transgenic plants having increased

XX tolerance to environmental stress as compared to wild type variety of


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RESULT 3

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AC ABN89809;

DT 18-SEP-2002 (first entry)

DE Physcomitrella patens GBP-1 partial cDNA sequence SEQ ID NO:1.

XX Physcomitrella patens; GBP; GTP binding protein; GBSRP; plant;
KM GTP binding stress-related protein; transgenic plant; agricultural;
KW environmental stress; salinity; drought; temperature; gene; se.

XX Physcomitrella patens.

OS US2002066124-A1.

PN 30-MAY-2002.

PD 06-APR-2001; 2001US-00828310.

PR 07-APR-2000; 2000US-0196001P.

XX (SIIV/) SIIVA O D C E.

PA (BOHN/) BOHNERT H J.

PA (THIE/) THIELEN N V.

PA (CHEN/) CHEN R.

PI Sliva ODCE, Bohnert HJ, Thiele N, Chen R;
XX WPI, 2002-556781/59.

XX Novel GTP binding stress-related proteins and genes encoding the
PT protein, useful for producing transgenic plants having increased
PT tolerance to environmental stress as compared to wild type variety of
PT plant cell.

XX Example 5; Fig 1A; 73p; English.

XX The present invention describes an isolated GTP binding stress-related
CC protein (GBSRP) (1) from Physcomitrella patens, selected from GTP binding
CC protein-1 (GBP-1), GBP-2, GBP-3, GBP-4 and GBP-5, or its orthologues. (1)
CC can be used for producing a transgenic plant (e.g. maize, wheat, rice,
CC oat, triticale, rice, barley, soybean, peanut, cotton, rapeseed, canola,
CC manhot, pepper, sunflower, tagetes, solanaceous plants, potato, tobacco,
CC eggplant, tomato, Vicia species, pea, alfalfa, coffee, cacao, tea, Salix
CC species, oil palm, coconut, perennial grass and forage crops). The
CC transgenic plants produced have increased tolerance to environmental
CC stresses (e.g. salinity, drought and temperature) as compared to a wild
CC type variety of the plant, from the plant cell. GBSRP polynucleotide
CC sequences can be used as markers for specific regions of the genome, and
CC also in functional studies of P. patens proteins. They can also be used
CC for evolutionary and protein structural studies. The present sequence
CC represents a P. patens GBP-1 partial cDNA sequence, which is used in the
CC exemplification of the present invention

SO Sequence 805 BP; 214 A; 218 C; 161 G; 212 T; 0 U; 0 Other;

Query Match 98.2%; Score 655; DB 6; Length 805;

Best Local Similarity 100.0%; Pred. No. 6.6e-216; Mismatches 0; Gaps 0;

Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 5 CGGTCCTGATGATCAAGAGCTGTGACATGTTCTCTGATGATGATTTTACGGCTTCT 64
DB 781 CGGTCCTGATGATCAAGAGCTGTGACATGTTCTCTGATGATGATTTTACGGCTTCT 722
QY 65 TGGGACATATGAGGCTGTGACAGAGAGGCCAAATCTGTTTCTGGGCTTCGACATGC 124
DB 721 TGGGACATATGAGGCTGTGACAGAGAGGCCAAATCTGTTTCTGGGCTTCGACATGC 662
QY 125 TGGCAAGACTACTCTTCTGACATGCTCAAGATGAGAACTGGGGCAATCAACCAAC 184
DB 661 TGGCAAGACTACTCTTCTGACATGCTCAAGATGAGAACTGGGGCAATCAACCAAC 602
QY 185 GCAGTATCCAGCTGACAGAGAGTGTGATCAACAGATGAAGTTCAAGCATTCATCT 244
DB 601 GCAGTATCCAGCTGACAGAGAGTGTGATCAACAGATGAAGTTCAAGCATTCATCT 542
QY 245 GGGTGGCCACAAATCGCTCGACGCGTGTGAGGAGCTACTATGCTAAGTGGATGCTAT 304
DB 541 GGGTGGCCACAAATCGCTCGACGCGTGTGAGGAGCTACTATGCTAAGTGGATGCTAT 482
QY 305 AGTATATCTGCTGACGACAGTGAACAGGAGATTTGCTGAGTCAAGAAAGAGCTCGA 364
DB 481 AGTATATCTGCTGACGACAGTGAACAGGAGATTTGCTGAGTCAAGAAAGAGCTCGA 422
QY 365 TTCTCTTCTCTCGAGAGATTTCTGTCCCAAGTTCTGTGCTCGTCTGGGAAACAAGAT 424
DB 421 TTCTCTTCTCTCGAGAGATTTCTGTCCCAAGTTCTGTGCTCGTCTGGGAAACAAGAT 362
QY 425 TGATATCCGTAAGCTTCTTCTGAAGAGAGTGGGTTCAACATTGGGTTGACATGAC 484
DB 361 TGATATCCGTAAGCTTCTTCTGAAGAGAGTGGGTTCAACATTGGGTTGACATGAC 302
QY 485 CACTGTAAAGAAAGCGTGAACCTGGGAGATGACAACTTGGCCCAATTGAGTTTCAT 544
DB 301 CACTGTAAAGAAAGCGTGAACCTGGGAGATGACAACTTGGCCCAATTGAGTTTCAT 242
QY 545 GTGCAATATTTGCGCAAAATGGGGTACGTTGAAGTTTCAAGTGAAGCCAGTACAT 604
DB 241 GTGCAATATTTGCGCAAAATGGGGTACGTTGAAGTTTCAAGTGAAGCCAGTACAT 182
QY 605 CAAGTATGTTTCTCTGAAAGAGAACTTACCTGCTGCTGTTTAAAGCGACGA 659
```

```
Db      181 CAAAGTATTGTTTCTGTGAAAAGAGAACTTAGCTCGGTGTTTAAGAGCGAGCA 127
RESULT 4
ADT91564/c
ID      ADT91564 standard; cDNA; 805 BP.
XX
AC      ADT91564;
XX
DT      16-DEC-2004 (first entry)
XX
DE      Physcomitrella patens GBSRP EST (expression sequence tag) partial cDNA.
XX
KM      GTP-binding stress-related protein; GBSRP; transgenic plant;
KM      environmental stress tolerance; stress resistance; cell metabolism; EST;
KM      expression sequence tag; ss.
XX
OS      Physcomitrella patens.
XX
PN      US2004194163-A1.
XX
PD      30-SEP-2004.
XX
PF      17-OCT-2003; 2003US-00688481.
XX
PR      07-APR-2000; 2000US-0196001P.
PR      06-APR-2001; 2001US-00828310.
XX
PA      (BADI ) BASF PLANT SCI GMBH.
XX
PI      Da Costa E Silveo, Bohnert HJ, Thieleen NV, Chen R;
XX
DR      WPI; 2004-698822/68.
XX
PT      Novel isolated nucleic acid encoding polypeptide e.g., GTP-binding stress
PT      related protein, useful for producing vector utilized for producing
PT      transgenic plant that has increased tolerance to environmental stress.
XX
PS      Example 5; SEQ ID NO 1; 62pp; English.
XX
CC      The invention relates to nucleic acid sequences encoding GTP-binding
CC      stress-related protein (GBSRP). GBSRP DNA is useful for producing a
CC      recombinant expression vector utilized for producing a transgenic plant
CC      that has increased tolerance to environmental stress, for identifying
CC      Physcomitrella patens and related organisms, for identifying and
CC      localising P. patens sequences of interest, for evolutionary studies, for
CC      determining GBSRP regions required for function, for modulating GBSRP
CC      activity, for modulating metabolism of one or more cell function, for
CC      modulating transport of one or more compounds, for modulating stress
CC      resistance or as markers for specific regions of the genome of P. patens.
CC      The present sequence is the Physcomitrella patens GBSRP EST (expression
CC      sequence tag) partial cDNA.
XX
SQ      Sequence 805 BP; 214 A; 218 C; 161 G; 212 T; 0 U; 0 Other;
Query March 98.24; Score 655; DB 13; Length 805;
Best Local Similarity 100.0%; Pred. No. 6,6e-216;
Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      5 CCGGTCCGTGATGATCAAGAGCTGTGACCATGTTCTTGATGATGTTTAAACGGCTTCT 64
DB      781 CCGGTCCGTGATGATCAAGAGCTGTGACCATGTTCTTGATGATGTTTAAACGGCTTCT 722
QY      65 TGCAGATAGGAGCTGTGCAAGAGAGGCCAAATCCGTTTCTGAGTCTGCAATGC 124
DB      721 TGCAGATAGGAGCTGTGCAAGAGAGGCCAAATCTGTTTCTGAGTCTGCAATGC 662
QY      125 TGCAGATAGTACTTCTTGTGACATGCTTCAAGATGAGAAATGCGGCAACATCAACCAAC 184
DB      661 TGCAGATAGTACTTCTTGTGACATGCTTCAAGATGAGAAATGCGGCAACATCAACCAAC 602
QY      185 GCAGTATCCAAAGCTCAAGAGAGTGAATATCAAGAGTGAAGTTCAAGATTCGATCT 244
```

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Db      601 GCAGTATCCAAAGCTCAGAGAGAGTTGATATCAACAGATGAAAGTTCAAGCATTCGATCT 542
QY      245 GGGTGGCCACACAATCGCTCGACGCGTGTGAGAGGACTATATGTAAGGTGATGCTAT 304
DB      541 GGGTGGCCACACAATCGCTCGACGCGTGTGAGAGGACTATATGTAAGGTGATGCTAT 482
QY      305 AGGTATATCTGCTGAGAGCGATGATACAGAGGAGAAATTTGCTGAGTCAAAAGAGCTCGA 364
DB      481 AGGTATATCTGCTGAGAGCGATGATACAGAGGAGAAATTTGCTGAGTCAAAAGAGCTCGA 422
QY      365 TTCTCTTCTCTCCGACGATCTCTGTCCCAAGTTCCGTGCTGCTCGTGGGAAACAAGAT 424
DB      421 TTCTCTTCTCTCCGACGATCTCTGTCCCAAGTTCCGTGCTGCTCGTGGGAAACAAGAT 362
QY      425 TGATATCCGTAAGCTTCTTGTGAAGACGATGCGGTTCACTTGTGAGTTGACATGAC 484
DB      361 TGATATCCGTAAGCTTCTTGTGAAGACGATGCGGTTCACTTGTGAGTTGACATGAC 302
QY      485 CACTGTGTAAGGAACGCTGAACCTGGGAGATACCAACTTCGGCCCATTTGAGTTTTCAT 544
DB      301 CACTGTGTAAGGAACGCTGAACCTGGGAGATACCAACTTCGGCCCATTTGAGTTTTCAT 242
QY      545 GTGCAATATTGTGCGCAAAATGGGGTACCGGTGAAGGTTTCAAGTGAATGCCAGTACAT 604
DB      241 GTGCAATATTGTGCGCAAAATGGGGTACCGGTGAAGGTTTCAAGTGAATGCCAGTACAT 182
QY      605 CAAAGTATTGTTTCTGTGAAAGAGAACTTACCTCGGTGTTTAAAGCGAGCA 659
DB      181 CAAAGTATTGTTTCTGTGAAAGAGAACTTACCTCGGTGTTTAAAGCGAGCA 127
RESULT 5
ABK71577
ID      ABK71577 standard; cDNA; 928 BP.
XX
AC      ABK71577;
XX
DT      30-JUL-2002 (first entry)
XX
DE      Human dlthp polynucleotide #43.
XX
KM      Human; dlthp; diagnostic and therapeutic polynucleotide; gene; ss; bone;
KM      cell proliferative disorder; cancer; tumour; autoimmune disorder; brain;
KM      inflammatory disorder; viral infection; bacterial infection; seizure;
KM      fungal infection; parasitic infections; developmental disorder; breast;
KM      endocrine disorder; metabolic disorder; neurological disorder; cervix;
KM      gastrointestinal disorder; transport disorder; gene therapy; kidney;
KM      adrenal gland; bone marrow; lung; ovary; pancreas; prostate; spleen;
KM      skin; testis; thymus.
XX
OS      Homo sapiens.
XX
PN      WO200220754-A2.
XX
PD      14-MAR-2002.
XX
PF      29-AUG-2001; 2001WO-US027127.
XX
PR      05-SEP-2000; 2000US-0229747P.
PR      05-SEP-2000; 2000US-0229748P.
PR      05-SEP-2000; 2000US-0229749P.
PR      05-SEP-2000; 2000US-0229750P.
PR      05-SEP-2000; 2000US-0229751P.
PR      05-SEP-2000; 2000US-0230583P.
PR      05-SEP-2000; 2000US-0230584P.
PR      05-SEP-2000; 2000US-0230585P.
PR      05-SEP-2000; 2000US-0230514P.
PR      05-SEP-2000; 2000US-0230515P.
PR      05-SEP-2000; 2000US-0230517P.
PR      05-SEP-2000; 2000US-0230518P.
PR      05-SEP-2000; 2000US-0230519P.
PR      05-SEP-2000; 2000US-0230595P.
PR      05-SEP-2000; 2000US-0230597P.
PR      05-SEP-2000; 2000US-0230598P.
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PR 06-SEP-2000; 2000US-0230599P.
PR 06-SEP-2000; 2000US-0230610P.
PR 06-SEP-2000; 2000US-0230655P.
PR 06-SEP-2000; 2000US-0230688P.
PR 07-SEP-2000; 2000US-0230951P.
PR 07-SEP-2000; 2000US-0231163P.
PR 07-SEP-2000; 2000US-0231167P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Stuart J, Lincoln SE, Altus CM, Dufour GE, Chalup MS, Hillman JL,
PI Jones AL, Yu JY, Wright RJ, Gietzen D, Liu TF, Yap PE, Dahl CR,
PI Momiyama MG, Bradley DL, Rohatgi SD, Harris B, Roseberry AM,
PI Gerstein EH, Peralta CH, David MH, Panzer SR, Flores V, Dafio A,
PI Marwaha R, Chen AJ, Chang SC, Au AP, Imman RR;
XX
XX MPI; 2002-383054/41.
XX P-PSDB; ABG59985.
XX
XX An isolated polynucleotide useful in diagnostics and therapeutics.
XX
XX Claim 1; Page 427; 686bp; English.
XX
XX The invention relates to human diagnostic and therapeutic (dthp)
XX polynucleotides and their associated polypeptides (DTHP polypeptides).
XX CC The sequences of the invention are used in the treatment and diagnosis of
XX CC cell proliferative disorders (e.g. atherosclerosis, cirrhosis), cancers
XX CC (e.g. tumours of the adrenal gland, bone, bone marrow, brain, breast,
XX CC cervix, kidney, lung, ovary, pancreas, prostate, skin, spleen, testis or
XX CC thymus), autoimmune/inflammatory disorders (e.g. asthma, bronchitis,
XX CC psoriasis, osteoporosis), viral infections, bacterial infections, fungal
XX CC infections, parasitic infections, developmental disorders (e.g. anaemia,
XX CC epilepsy), seizure disorders (e.g. cerebral palsy, spina bifida),
XX CC endocrine disorders (e.g. thrombosis, aneurysm), metabolic disorders
XX CC (e.g. obesity, diabetes), neurological disorders (e.g. stroke,
XX CC amyotrophic lateral sclerosis, multiple sclerosis), gastrointestinal
XX CC disorders (e.g. ulcerative colitis, lysinuria) and transport disorders
XX CC (e.g. myotonic dystrophy, catatonla, peripheral neuropathy). Sequences
XX CC ABK71535-ABK71809 represent human dthp polynucleotides of the invention
XX
XX Sequence 928 BP; 206 A; 251 C; 262 G; 209 T; 0 U; 0 Other;
SQ
Query Match 51.0%; Score 340.4; DB 6; Length 928;
Best Local Similarity 74.7%; Pred. No. 1e-106;
Matches 441; Conservative 0; Mismatches 146; Indels 3; Gaps 1;
QY 23 GGCTGTACCATGTTCTTGTAGATTGTTTACGGCTTCTTTCGAGCATAGAGGCTGTG 82
DB 153 GGTGGGGAGATGTTCTCTGAGACTGTTCTACGGGGTCTGCTCCCTCGGCTGTG 212
QY 83 GCAGAGGAGGCGCAAAATCTGTTTGGGCTTCGACATGTCGCAAGACTACTTCT 142
DB 213 GCAGAGGAGGCGCAAAATCTTCTTCTTCTGCTTCGACAGCCGCGCAAGCGTGTCT 272
QY 143 GCACATGCTCAAGATGAGAAATCTGGGCGCAATCAACCAAGCAGATCAAGTCAAG 202
DB 273 CCACATGCTCAAGAGACGCGGTTGTGCGACCAAGCCAGCAGCAGCGTGTGGA 332
QY 203 GGAATTGATGATCAACAGAGTGAAGTTCAAGATTCGATCTGGTGGCCACAATCGC 262
DB 333 GGAATCAGATCGGCAAGATCAAGTCAAGGCTTCGACCTCGGGGCGCACCAAGATCG 382
QY 263 TCACACCGGTGTGAGGAGCTACTATGTCTAAGGTGATGCTATGTCTGTCAAGC 332
DB 393 GCCCGCGTGTGAGAGATTAACGCAAGGTTGATGCTGTAGTACTGTGTAGATGC 452
QY 323 AGTAGACAGGAGGATTTGCTGATCAAGAAAGAGCTGATTTCTTCTCCGACGA 382
DB 453 ATATGATTAAGACGAGATTTCTGATTAAGAAAGAGCTGATGCTTCTGTCTATGA 512
QY 383 TTCTGTCTCCCAAGTTCTGTGCTGTGCTGTGAGAAACAGATGATATCCCGTACGCTTC 442
DB 513 TTCTTTGGCCAAAGTTCTCATTTCTCATCTTGGCAACAAATGATATCCCATATGCTGC 572

QY 443 TTCTGAAGACGAGTTCGGTTCACATTGGGTTGACCA---TGACCATCTGTAAAGAAC 499
DB 573 CTCTGAAGACGAGCTACAGCTATCACCTTAGCAGCTTACCAACACGGGAGGCA 632
QY 500 GGTGAACCTGGAGATGACATTCGGCCCATTTGAGCTTTTCATGTGCGATTTGGCG 559
DB 633 GGTCAACCTTGGCGCATCTCCATGTCCTTCACTTGAAGGTCTTCATGTGCGATTTGGCG 692
QY 560 CAAATGGGTACCGGTGAAGTTTCAAGTGATGACCCAGTACATCAAGT 609
DB 693 CAAGATGGGCTACGGATGATGTTTCAAGTGGGTCTTCCAGTACATCAAGT 742
RESULT 6
ADX12667
ID ADX12667 standard; cDNA; 998 BP.
XX
XX ADX12667;
XX
XX 21-APR-2005 (first entry)
XX
XX Plant full length insert polynucleotide seqid 7242.
XX
XX plant protectant; plant growth regulant; gene therapy; plant;
XX KM recombinant DNA construct; physical array; plant breeding marker;
XX KM cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
XX KM extreme osmotic condition; pathogen tolerance; pest tolerance;
XX KM growth rate; cell cycle pathway; disease resistance;
XX KM galactomanan production; lignin production; plant growth regulator;
XX KM yield; plant growth; plant development; seed oil; protein yield;
XX KM protein content; gene; ss.
XX
XX Unidentified.
XX
XX US2004034888-A1.
XX
XX 19-FEB-2004.
XX
XX 28-APR-2003; 2003US-00425114.
XX
XX 06-MAY-1999; 99US-00304517.
XX PR 05-NOV-2001; 2001US-00985678.
XX
XX (LIU/) LIU J.
XX PA (ZHOU/) ZHOU Y.
XX PA (KOVA/) KOVALIC D K.
XX PA (SCRE/) SCREEN S E.
XX PA (TAB/) TABASKA J E.
XX PA (CAO/) CAO Y.
XX
XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y,
XX MPI; 2004-180133/17.
XX
XX New recombinant DNA construct, useful for improving plant tolerance to
XX PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
XX PT pests, for conferring increased resistance to plant disease, or for
XX PT improving yield.
XX
XX Claim 1; SEQ ID NO 7242; 15pp; English.
XX
XX The invention describes a recombinant DNA construct comprising a
XX CC polynucleotide consisting of a sequence encoding an amino acid sequence
XX CC available in electronic form from the US patent office at
XX CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
XX CC of the invention are also useful in physical arrays of molecules and as
XX CC plant breeding markers. The recombinant DNA construct is useful for
XX CC improving plant tolerance to cold, heat, drought, herbicides, extreme
XX CC osmotic conditions, pathogens or pests, for manipulating growth rate in
XX CC plant cells by modification of the cell cycle pathway, for conferring
XX CC increased resistance to plant disease, for producing galactomanan,
XX CC lignin or plant growth regulators, for increasing the rate of homologous

CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This sequence represents a plant full length insert
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.

XX
SQ Sequence 998 BP, 225 A, 266 C, 269 G, 238 T, 0 U, 0 Other;

Query Match 51.0%; Score 340.4; DB 13; Length 998;

Best Local Similarity 74.7%; Pred. No. 1.1e-106; Mismatches 146; Indels 3; Gaps 1;

Matches 441; Conservative 0; Mismatches 146; Indels 3; Gaps 1;
QY 23 GCGTGTACCATGTTCTTGTAGATTGTTTACGCTTTCTTTCGAGCATAGAGGCTGTG 82
DB 156 GGTGGGGAATGTTCTCTGGAGCTGTTCTACGGGGTGTCTGGCTCCCTCGGCTGTG 215
QY 83 GCAGAAAGAGCCAAATCTCTGTTTCTGGGCTTCGACAAATGCTGGCAAGTACTCTTCT 142
DB 216 GCAGAAAGAGCCAAAGTCTCTTCTTGGCTTCGACAAAGCCGCGCAAGCAGCTGCT 275
QY 143 GCACATGCTCAAGGATGAAACTGGGGCAACATCAACCAAGCATTCACAGTCA 202
DB 276 CCACATGCTCAAGGACGAGCGGTTGTGACACACACGACGACGACGAGCTCGA 335
QY 203 GGAAGTGTATCAACAGAGTGAAGTTCAAGCATTTGATCTGGGTGGCCACAAATGCG 262
DB 336 GGAAGTGTATGCGCAAGATCAAGATTCAGAGGCTTCGACCTGGGCGGCCACAGATCG 395
QY 263 TCGACGCGTGTGAGGAGCTACTATGCTAAGTGGATGCTATGATCTCTGTCAGCG 322
DB 396 GCGCGCGGTGTGAAAGATTAACGCAAGGTTGATGCTGTAGTAACTGTGAGATGC 455
QY 323 AGTAGACAGGAGAGATTTCGTGAGTCAAGAAAGAGCTGATCTCTCTCCGACGA 382
DB 456 ATATGATAGAGAGGATTTGCTGATTAAGAAAGAGCTGATCTCTCTCTGATGA 515
QY 383 TTCTCTGCCAAGTTCTGTGCTGCTCTGCGAACAAGATTGATATCCCGTACGCTTC 442
DB 516 TTCTTTGGCCAAAGTTCATTTCTCATCTTGGCAACAAGATTGATATCCCATATGCTGC 575
QY 443 TTCTGAAAGAGAGTTGGGCTTACACTTGGTTGACCA---TGACCACTGTGTAAGAAC 499
DB 576 CTCTGAAAGAGAGCTACGATACCTTAAGGCTTGAACCTTCAACACCGGGAAGGCA 635
QY 500 GGTGAACCTGGGAGATGCAACATTTGGCCATTGAGGTTTCAATGACAGTATTGCG 559
DB 636 GGTCAACCTTTGGCGAATCTCCATGTCCTGCTCACTTGAAGGCTTTCATGTCAGTGTTCG 695
QY 560 CAAATGCGGTACCGTGAAGTTTCAAGTGGATGACCAAGTACATCAAGT 609
DB 696 CAAAGTGGGCTACGATGATGTTTCAAGTGGGCTCCCAAGTACATCAAGT 745

RESULT 7
ADX46899
ID ADX46899 standard; cDNA, 955 BP.

XX
AC ADX46899;

XX
DT 21-APR-2005 (first entry)

XX
DE Plant full length insert polynucleotide seqid 21639.

XX
KM plant protectant; plant growth regulator; gene therapy; plant;
KM recombinant DNA construct; physical array; plant breeding marker;
KM cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KM extreme osmotic condition; pathogen tolerance; pest tolerance;
KM growth rate; cell cycle pathway; disease resistance;
KM galactomannan production; lignin production; plant growth regulator;
KM yield; plant growth; plant development; seed oil; protein yield;
KM protein content; gene; ss.

XX
OS Unidentified.
XX
PN US2004034888-A1.

XX
PD 19-FEB-2004.

XX
PF 28-APR-2003; 2003US-00425114.

XX
PR 06-MAY-1999; 99US-00304517.

XX
PR 05-NOV-2001; 2001US-00985678.

XX
PA (LIU/) LIU J.

XX
PA (ZHOU/) ZHOU Y.

XX
PA (KOVA/) KOVALIC D. K.

XX
PA (SCRE/) SCREEN S E.

XX
PA (TAB/) TABASKA J E.

XX
PA (CAO/) CAO Y.

XX
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;

XX
PI MPI; 2004-180133/17.

XX
PS Claim 1; SEQ ID NO 21639; 15bp; English.

XX
CC The invention describes a recombinant DNA construct comprising a

XX
CC polynucleotide consisting of a sequence encoding an amino acid sequence

XX
CC available in electronic form from the US patent office at

XX
CC ftp://seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide

XX
CC of the invention are also useful in physical arrays of molecules and as

XX
CC plant breeding markers. The recombinant DNA construct is useful for

XX
CC improving plant tolerance to cold, heat, drought, herbicides, extreme

XX
CC osmotic conditions, pathogens or pests, for manipulating growth rate in

XX
CC plant cells by modification of the cell cycle pathway, for conferring

XX
CC increased resistance to plant disease, for producing galactomannan,

XX
CC lignin or plant growth regulators, for increasing the rate of homologous

XX
CC recombination in plants, for improving yield by modification of

XX
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake

XX
CC or by providing improved plant growth and development under at least one

XX
CC stress condition or for modifying seed oil or protein yield and/or

XX
CC content. This sequence represents a plant full length insert

XX
CC polynucleotide that can be used in the recombinant DNA construct of the

XX
CC invention.

XX
SQ Sequence 955 BP, 219 A, 222 C, 289 G, 225 T, 0 U, 0 Other;

Query Match 50.3%; Score 335.6; DB 13; Length 955;

Best Local Similarity 73.7%; Pred. No. 4.9e-105; Mismatches 154; Indels 3; Gaps 1;

Matches 441; Conservative 0; Mismatches 154; Indels 3; Gaps 1;

QY 19 CCAAGCTGTACCATGTTCTTGTAGATTGTTTACGAGCTTCTTTCGAGCATAGAGC 78
DB 84 CCGAGTTGTAAGATGTTCTCTGTGAGCTGTTTATGAGGGGTGGCATCTCGGCG 143
QY 79 TGTGGCAGAAAGAGGCGCAAAATCTCTTCTGTGGGTCTCGACAAATGCTGGCAAGACTATC 138
DB 144 TGTGGCAGAAAGAGGCTTAAGATCTCTCTTGGCCCTCGACAAAGCCGGAAGCAACC 203
QY 139 TTCTGCACATGCTCAAGATGAGAAACTGGGGCAACATCAACCAAGCAGATATCAAGT 198
DB 204 TCCTTCACATGCTGAAGAGAGAGCGGCTGTAAGACACAGCCACGACATACCCACGT 263
QY 199 CAGAGAGTTGAGTATCAACAGAGTGAAGTTCAAGAGCTTGTGAGTGGGCCACACAA 258
DB 264 CAGAGAGTTGAGCATCGGCAAGATCAAGTTCAAGGGGTTGACCTTGGGGCCACAGA 323
QY 259 TCGCTGACCGGTGTGAGGAGACTACTATGCTAAGGTGATGCTATAGTATCTCTCTG 318

DB 324 TCCGCCGCCGCTGTGGAAGACTACGACCAAGGTGATGCTGTGTGTAATTGTG 383
QY 319 ACGCAGTAGACAGAGGAGATTGTGAGTCGAAGAAAGAGCTGATTCCTTCTCCG 378
DB 384 ATGCTGTGACAGGAACGTTTGGCCGAGTCGAAGAGAGCTGATGCGCTTCTGCA 443
QY 379 ACGATTCTGTGTCACCAAGTTCCTGTGCTGCTCCGAGAAACAGATTGATATCCGTAC 438
DB 444 ATGACCTCCCTGGAACGTTTCTTCTCTCACTATCGGCAACAGATTGATCCCAAG 503
QY 439 CTTCTTCTGAAGACGAGTTGCGGTTCACCTGGGTTGACCA--TGACCACTGTGAAG 495
DB 504 CGGCTTCAGAGGAGAGCTGAGTACTACCTCGGCTGAGCACTTCACAAACCGGGAAG 563
QY 496 GAACGGTGAACCTGGAGATAGCAACATTCGCGCCATGAGTTTCATGTGAGTATG 555
DB 564 GCAACGTGAACCTGGAGCTGACCAAGCTCCGCCCCCTGAGATCTTCAATGCAAGTGTG 623
QY 556 TCGCAGAAATGGGGTACGAGTGAAGTTTCAAGTGAATGACCACTACATCAAGTAT 613
DB 624 TCGCAAGATGGGCTATGGGGAAGGCTTCAATGATGTCTCAATCAATCAAGT 681

RESULT 8
AD30716
ID AD30716 standard; cDNA; 966 BP.
XX
AC AD30716;
XX
DT 21-APR-2005 (first entry)
XX
DE plant full length insert polynucleotide seqid 13536.
XX
KW plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content; gene; ss.
XX
OS unidentified.
XX
PN US2004034888-A1.
XX
PD 19-FEB-2004.
XX
PF 28-APR-2003; 2003US-00425114.
XX
PR 06-MAY-1999; 99US-00304517.
XX
PR 05-NOV-2001; 2001US-00985678.
XX
PA (LIU/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D. K.
PA (SCRE/) SCREEN S. E.
PA (TAB/) TABASKA J. E.
PA (CAO/) CAO Y.
XX
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX
XX WPI; 2004-180133/17.
XX
DR
PT New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
XX Claim 1; SEQ ID NO 13536; 15bp; English.
XX
CC The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence

CC available in electronic form from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This sequence represents a plant full length insert
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.
XX
SQ Sequence 966 BP; 225 A; 218 C; 294 G; 229 T; 0 U; 0 Other;
XX
Query Match 49.8%; Score 332.4; DB 13; Length 966;
Best Local Similarity 73.4%; Pred. No. 6,3e-104;
Matches 429; Conservative 0; Mismatches 156; Indels 3; Gaps 1;
QY 19 CCAAGGCTGTGACCAATGTTCTGTGATGATGCTTTTACGCTTTTGGAGCATAGGC 78
DB 116 CCGAGTTGTAAAGATGTTCTGTGAGTGTGCTATGAGGGGTGCTGCATCGCTTGGGC 175
QY 79 TGTGGCAGAGAGGCGCAAAATCTGTTTCTGGGTTCGACAAATGCTGGCAAGACTATC 138
DB 176 TGTGGCAGAGAGGCTTAAGATCTTCTTCTTGGCTTCACAAACGCGGCAAGACACC 235
QY 139 TTTGTGACATGCTCAAGATGAGAAACGCGGCAACATGACCAACGAGTATCAACGT 198
DB 236 TCTCTCAATGCTGAAGAGCAAGCGGCTGTACAGCACGCGACGAGTACCCACGT 295
QY 199 CAGAGGATGTGATTCACAGAGTGAAGTTCAGAAATTCATGCTGAGTGGCCACACA 258
DB 296 CAGAAGATGTGAGCATTCGCAAGATTAAGTTCAGAGCGTTGACCTTGGGGGCAACAG 355
QY 259 TGTGTCAGCGCGTGTGAGAGCACTACTATGCTAAGTGAATGTATAGTATCTGTG 318
DB 356 TCGCCCGCGCGCTGTGGAAGCACTACTACGCAAGGTATGTGTGTACTTGTGTG 415
QY 319 ACGCAGTAGACAGAGGAGATTTGCTGAGTCAAGAAAGAGCTGATTCCTTCTCCG 378
DB 416 ATGCTGTGACAGAGAACGTTTGGCCGAGTCAAGAGAGCTTGATGCGCTTCTGCA 475
QY 379 ACGATTCTGTGCCAAGTTCCTGTGCTGCTGCTGGGAAACAGATTGATATCCGTAC 438
DB 476 ATGACTCCCTTGAACAGTTCCTTCTCTCACTATCGGCAACAGATTGATCCCAAG 535
QY 439 CTTCTTCTGAAGACGAGTTGCGGTTCACCTTGGGTTGACCA--TGACCACTGTGAAG 495
DB 536 CGGCTTCAGAGAGAGAGCTGAGGTACTACCTCGGCTGAGCAACTTCACAAACCGGGAAG 595
QY 496 GAACGGTGAACCTGGAGATAGCAACATTCGCGCCATTGAGTTTCATGTGAGTATG 555
DB 596 GCAACGTGAACCTGGCCGAGCTCCAAATGCGGCGCTGAGAGTCTTCAATGCAAGTGTG 655
QY 556 TCGCAGAAATGGGGTACGAGTGAAGTTTCAAGTGAATGACCACTACATCAAGTAT 613
DB 656 TCGCAAGATGGGCTATGGCGAAGGCTTCAATGATGTCTCAATCAATCAAGT 713

RESULT 9
AD30716
ID AD30716 standard; cDNA; 1017 BP.
XX
AC AD30716;
XX
DT 21-APR-2005 (first entry)
XX
DE plant full length insert polynucleotide seqid 33380.

XX plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content; gene; ss.
XX
OS Unidentified.
XX
XX US2004034888-A1.
XX
XX 19-FEB-2004.
XX
XX 28-APR-2003; 2003US-00425114.
XX
XX 06-MAY-1999; 99US-00304517.
XX
XX 05-NOV-2001; 2001US-00985678.
XX
XX (LIU//) LIU J.
XX (ZHOU//) ZHOU Y.
XX (KOVA//) KOVALIC D. K.
XX (SCRE//) SCREEN S. E.
XX (TABAS//) TABASKA J. E.
XX (CAO//) CAO Y.
XX
XX Liu J., Zhou Y., Kovalic DK., Screen SE., Tabaska JE., Cao Y.;
XX WPI; 2004-180133/17.
XX
XX New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
XX Claim 1; SEQ ID NO 33380; 15pp; English.
XX
XX The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp://seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This sequence represents a plant full length insert
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.
XX
XX Sequence 1017 BP; 229 A; 229 C; 311 G; 248 T; 0 U; 0 Other;
SQ
Query Match 49.8%; Score 332.4; DB 13; Length 1017;
Best Local Similarity 73.4%; Pred. No. 6.5e-104;
Matches 439; Conservative 0; Mismatches 156; Indels 3; Gaps 1;
QY 19 CCAAGCTGTGATCCATGTTCTTGAGATGGTTTACGGCTTCTTGCGAGCATAGGGC 78
DB 97 CCGAGGTGTAAAGATGTTCTGTGAGCTGTTCTAAGGGCTCTGCGATCGCTTGGGC 156
QY 79 TGTGGCAGAGAGAGAGCCAAATCTGTTCTGGGCTTCGACATGCTGGCAAGACTATC 138
DB 157 TGTGGCAGAGAGAGAGCTAAGATCTCTTCTTGCTTGGCTTGAAGAGCGGCAAGCACCC 216
QY 139 TTTCGACATGCTCAAGAGATGAGAACTGGGGCAACATCAACCAACGATATCCAACT 198

DB 217 TCTCTACATGCTGAAGAGCGAGCGGCTCTACAGACCAAGCCGAGCGATACCCACGT 276
QY 199 CAGAGAGATTGATATCAACAGATGAGATTCAGAAACATTCGATCGGTGGCCACACA 258
DB 277 CAGAAAGTTGAGATTCGACAGGATCAAGTTCAAGCGTTTGAAGCTTGGGGGGCCACAGA 336
QY 259 TCGCTGACGCGGTGTGAGAGGACTACTATGCTAAGGTGATGCTATAGTATCTGTGTG 318
DB 337 TCGCCCGCGCGTCTGGAAGGACTACTACGCCAAGGTTATGCTGTGTGTACTTGGTGTG 396
QY 319 AGCGGTAGACAGGAGAGATTTGCTGAGTCAAGAAAGAGCTCGATTCTTCTCTCCG 378
DB 397 ATGCTGTGACAGAGAACCTTTTGGCCGAGTCGAGAGAGAGCTTGATGGCTTCTTCCAG 456
QY 379 ACGATTCTGTCCTCCAGTTCTCTGCTGCTGCTGCGAAACAGATTGATATCCCGTAGC 438
DB 457 ATGACTCCCTTGGAAACGTTCTTCTCTATCTAGTGGGCAACAGATTGACATCCATAG 516
QY 439 CTTCTTCTGAAAGACGATTGCGGTTCAACATTGGGTTGACCA--TGACCACTGTAAAG 495
DB 517 CCGCTTCAAGAGAGAGCTGAGGTACTACTCTGCGCTGAGCAACTTCACAAACCGGAGAG 576
QY 496 GAAACGTTGAACCTGGAGATAGCAATTCGGGCCATTGAGGTTTCATGTGAGATTTG 555
DB 577 GCAACGTGAACCTTGGCCGACTCCAAATGTCGGGCCCTGGAGATCTTCATGTGAGTGG 636
QY 556 TGGCAGAAATGGGGTACGGTGAAGTTTCAAGTGATGACCCAGTACATCAAGTATT 613
DB 637 TGGCAGAGATGGCTATGGCGAAGGCTTCAATGATGTCTGATGATCAATCAAGTAGT 694
RESULT 10
ADM45502
ID ADM45502 standard; DNA; 811 BP.
XX
XX ADM45502;
XX
XX 03-JUN-2004 (first entry)
XX
XX Insect resistance associated DNA sequence SeqID909.
XX
XX Insect resistant phenotype; plant protectant; gene therapy;
KW Arabidopsis thaliana; Nicotiana benthamiana; Oryza sativa;
KW Papaver rhoeas; rice; insect resistance; insect-resistant plant; ds.
XX
XX Unidentified.
XX
XX WO2003020025-A2.
XX
XX 13-MAR-2003.
XX
XX 30-AUG-2002; 2002WO-US027882.
XX
XX 31-AUG-2001; 2001US-0316319P.
XX
XX (DOWC) DOW CHEM CO.
XX
XX Shukla V., Meade T., Larrinua I;
XX
XX WPI; 2003-290133/28.
XX
XX New isolated nucleic acid having expression that results in an insect
PT resistant phenotype, useful for conferring insect resistance and for
PT producing insect-resistant plants.
XX
XX Claim 1; SEQ ID NO 909; 396pp; English.
XX
XX This invention relates to a novel isolated nucleic acid comprising, or
CC hybridizing under low stringent conditions to, any of the 1214 nucleic
CC acid sequences given in the specification, where the expression of the
CC nucleic acid in a plant results in an insect resistant phenotype. The
CC invention may be useful as a plant protectant or for gene therapy. The

CC genes are derived from *Arabidopsis thaliana*, *Nicotiana benthamiana*, *Oryza sativa* and *Papaver rhoeas*. The isolated nucleic acid and vector are useful for conferring insect resistance and for producing insect-resistant plants. The present sequence is that of a DNA sequence of the invention which may confer insect resistance to plants.

CC Sequence 811 BP; 219 A; 157 C; 199 G; 236 T; 0 U; 0 Other;

Query Match 49.7%; Score 331.2; DB 11; Length 811;

Best Local Similarity 73.6%; Pred. No. 1.5e-103;

Matches 436; Conservative 0; Mismatches 153; Indels 3; Gaps 1;

```

Oy 28 GTCACATGTTCTTCTAGATGGTTTACGGCTTCTTGGACATAGGCGTGGCAGA 87
    |||||
Db 126 GCACAGTGTCTTCTGATGATGGTTTCTATGGAATTTAGCAAGCTCGGATTTAGCAGA 185
    |||||
Oy 88 AGAGGCGCAAAATCTGTTCTGAGTCTCGACATGCTGGCAAGACTCTTCTGCACA 147
    |||||
Db 186 AGAGGCGTAAGATCTGTTTGGGCTCGATATGCGGCAAAACCACTTACTCATTA 245
    |||||
Oy 148 TGCTCAAGATGGAAGATCGGGCAATACCAACGCGATTCACAGTCCAGAGAGT 207
    |||||
Db 246 TGTGAAAGATGAGAGATGTTTCAATCAGCAACACAAATTCGACCTCAGAGAGC 305
    |||||
Oy 208 TGAGTATCAACAGATGAAGTCAAAAGCATTCGATCGGTGGCCACAAATGCTCGAC 267
    |||||
Db 306 TTGATATCGGCAAGATCAAGATTCAAAGCATTTGATCGGTGGTCAATCAATTCGCGC 365
    |||||
Oy 268 GCGTGTGAGGAGCTACTATGCTAAGTGTGATCTATGATCTCTGTCAGCAGTAG 327
    |||||
Db 366 GTGTTTGAAAGATTTATGATGATGATGATGATGATGATGATGATGATGATGATG 425
    |||||
Oy 328 ACAGGAGAGATTTCTGAGTCAAGAAAGCTCGATTTCTTCTCTCGAGATTC 387
    |||||
Db 426 ACAAGAGAGATTTCTGAGTCAAGAAAGCTCGATTTCTTCTCTCGAGATTC 485
    |||||
Oy 388 TGTCCCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 447
    |||||
Db 486 TGGCAACTGTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 545
    |||||
Oy 448 AAGACGAGTTCGCTTCAACATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 504
    |||||
Db 546 AAGATGAGTTCGCTTCAACATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 605
    |||||
Oy 505 ACCTGGAGATGACAAATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 564
    |||||
Db 606 ACCTGGAGATTCGCTTCAACATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 665
    |||||
Oy 565 TGGGGTACGCTGAGATTTCAAGTGTGATGCCAGTATCAATCAATGATTTGTT 616
    |||||
Db 666 TGGGATATGAGAGAGCTTCAAGTGTGATGCCAGTATCAATCAATGATTTGTT 717
    |||||
```

RESULT 11

ID ADM45760 standard; DNA; 830 BP.

AC ADM45760;

DT 03-JUN-2004 (first entry)

XX Insect resistance associated DNA sequence SegID1167.

XX Insect resistant phenotype; plant protectant; gene therapy;

XX *Arabidopsis thaliana*; *Nicotiana benthamiana*; *Oryza sativa*;

XX *Papaver rhoeas*; rice; insect resistance; insect-resistant plant; ds.

OS Unidentified.

XX WO2003020025-A2.

XX PD 13-MAR-2003.

PF 30-AUG-2002; 2002WO-US027882.

XX 31-AUG-2001; 2001US-0316319P.

XX (DOWC) DOW CHEM CO.

XX Shukla V, Meade T, Laxrinnua I;

XX MPI, 2003-290133/28.

DR New isolated nucleic acid having expression that results in an insect

PT resistant phenotype, useful for conferring insect resistance and for

PS producing insect-resistant plants.

XX Claim 1; SEQ ID NO 1167; 396bp; English.

XX This invention relates to a novel isolated nucleic acid comprising, or

CC hybridizing under low stringent conditions to, any of the 1214 nucleic

CC acid sequences given in the specification, where the expression of the

CC nucleic acid in a plant results in an insect resistant phenotype. The

CC invention may be useful as a plant protectant or for gene therapy. The

CC genes are derived from *Arabidopsis thaliana*, *Nicotiana benthamiana*, *Oryza*

CC *sativa* and *Papaver rhoeas*. The isolated nucleic acid and vector are

CC useful for conferring insect resistance and for producing insect-

CC resistant plants. The present sequence is that of a DNA sequence of the

CC invention which may confer insect resistance to plants.

Sequence 830 BP; 221 A; 165 C; 204 G; 240 T; 0 U; 0 Other;

Query Match 49.7%; Score 331.2; DB 11; Length 830;

Best Local Similarity 73.6%; Pred. No. 1.5e-103;

Matches 436; Conservative 0; Mismatches 153; Indels 3; Gaps 1;

```

Oy 28 GTCACATGTTCTTCTAGATGGTTTACGGCTTCTTGGACATAGGCGTGGCAGA 87
    |||||
Db 145 GCACAGTGTCTTCTGATGATGGTTTCTATGGAATTTAGCAAGCTCGGATTTAGCAGA 204
    |||||
Oy 88 AGAGGCGCAAAATCCGTTTCTGAGTCTCGACATGCTGGCAAGACTCTTCTGCACA 147
    |||||
Db 205 AGAGGCGTAAGATCTGTTTGGGCTCGATATGCGGCAAAACCACTTACTCATTA 264
    |||||
Oy 148 TGCTCAAGATGGAAGATCGGGCAATACCAACGCGATTCACAGTCCAGAGAGT 207
    |||||
Db 265 TGTGAAAGATGAGAGATGTTTCAATCAGCAACACAAATTCGACCTCAGAGAGC 324
    |||||
Oy 208 TGAGTATCAACAGATGAAGTCAAAAGCATTCGATCGGTGGCCACAAATGCTCGAC 267
    |||||
Db 325 TTGATATCGGCAAGATCAAGTTCAAAGCATTTGATCGGTGGTCAATCAATTCGCGC 384
    |||||
Oy 268 GCGTGTGAGGAGCTACTATGCTAAGTGTGATCTATGATCTCTGTCAGCAGTAG 327
    |||||
Db 385 TGTCCCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 444
    |||||
Oy 328 ACAGGAGAGATTTCTGAGTCAAGAAAGCTCGATTTCTTCTCTCGAGATTC 387
    |||||
Db 445 ACAAGAGAGATTTCTGAGTCAAGAAAGCTCGATTTCTTCTCTCGAGATTC 504
    |||||
Oy 388 TGTCCCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 447
    |||||
Db 505 TGGCAACTGTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 564
    |||||
Oy 448 AAGACGAGTTCGCTTCAACATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 504
    |||||
Db 565 AAGATGAGTTCGCTTCAACATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 624
    |||||
Oy 505 ACCTGGAGATGACAAATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 564
    |||||
Db 625 ACCTGGAGATTCGCTTCAACATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 684
    |||||
Oy 565 TGGGGTACGCTGAGATTTCAAGTGTGATGCCAGTATCAATCAATGATTTGTT 616
    |||||
Db 685 TGGGATATGAGAGAGCTTCAAGTGTGATGCCAGTATCAATCAATGATTTGTT 736
    |||||
```

RESULT 12
AEB67368
ID AEB67368 standard; DNA; 952 BP.
AC AEB67368;
XX
XX
DT 22-SEP-2005 (first entry)
XX
XX Rice genome derived DNA sequence, SEQ ID 2513.
DE
XX
XX transcription; gene regulation; transgenic plant; RNA interference;
KM transformation; antibody; ds.
XX
XX Oryza sp.
OS
XX JP2005185101-A.
PN
XX 14-JUL-2005.
XX
XX 11-DEC-2002; 2002JP-00383870.
PF
XX 30-MAY-2002; 2002JP-00203269.
PR
XX (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
PA (SEIB-) SEIBUTSUKAI TOKUTEI SANGYO GIJUTSU.
PA (DOKU-) DOKURITSU GYOSEI HOJIN RIKAGAKU KENKYUSH.
PA (KOKU-) ZH KOKUSAI KAGAKU SHINKO ZAIDAN.
XX
XX Kikuchi H, Hayashizaki Y, Otsomo Y, Matsubara K, Murakami K,
PI Kishimoto N, Sato K, Nagata T, Kawakami N, Yazaki J, Ishikawa M,
PI Doi K, Kawai J;
XX WPI; 2005-566181/58.
XX
XX Novel DNA encoding transcription factor, derived from rice plant, useful
PT for obtaining transcriptional-regulatory regions in plant and for
PT producing modified plant.
XX
XX Claim 1; SEQ ID NO 2513; 2928bp; Japanese.
XX
XX The invention relates to a novel DNA sequence encoding a transcription
CC factor derived from a plant. The invention further comprises antisense
CC RNA sequences, ribozyme activity RNA, RNAi sequences, a vector,
CC transformed plant cells, antibodies and proteins, all related to the
CC novel plant DNA sequences of the invention. The novel DNA is preferably
CC derived from a rice-genome database. The invention further provides a
CC method for determining the transcription regulatory regions of the rice
CC genome. The novel DNA is useful for controlling the expression of a gene
CC in a plant and for producing a modified plant with desired and different
CC characteristics. The plant DNA and method enables the acquisition of many
CC transcriptional-regulatory regions. This polynucleotide represents a DNA
CC sequence taken from a rice genome clone library for use in the invention.
CC Note: This sequence is not shown in the specification. It has been
CC retrieved from a sequence listing in electronic format from the Japanese
CC Patent Office. The invention claims DNA sequences of SEQ ID Nos 1 to
CC 28469 and encoded protein sequences of SEQ ID Nos 28470 to 56791,
CC however, the sequence listing only provided the DNA sequences of SEQ ID
CC Nos 1 to 3032.
XX
XX
SQ Sequence 952 BP; 209 A; 248 C; 272 G; 223 T; 0 U; 0 Other;
Query Match 49.5%; Score 330.4; DB 14; Length 952;
Best Local Similarity 74.3%; Pred. No. 3,1e-103;
Matches 431; Conservative 0; Mismatches 146; Indels 3; Gaps 1;
QY 33 ATGTTCTTGTAGATTGCTTTTACGCTTTTCGAGCATAGGCTGTGCGAGAGAG 92
DB 130 ATGTTCTGCTGAGCTGCTTCTACGCGGGTGTGCTGCGCTGTGCGAGAGAG 189
QY 93 GCGAAATCCGTTCTTGGGCTCTGACATGCTGCGAGAGATCTCTTTCGACATGTC 152
DB 190 GCGAAGATCTTCTCTGCGCTGACAAAGCGCGGCAAGACCAAGCTCTCTCAATGCTC 249

QY 153 AAGATGAGAAATGGGGCAACATCAACCAAGCAGTATTCACAGCTCAGAGAGTTGACT 212
DB 250 AAGACGAGAGATTGGTGAAGCATCAACCTACCACTATCCGACTTCTGAAGAGCTGAGC 309
QY 213 ATCAACAGATGAAGTTCAAAAGCATTCGATCTGGGGGCGACACATTCGCTGACGCGTG 272
DB 310 ATTGGGAAGATCAAGTTCAAGGCGCTTTGATTTTGAAGGCCATATMAATTGCTCCCGTGTG 369
QY 273 TGAAGGAGCTACTATCTATAGTGAATGCTATAGTATCTCGTCGACGAGTAGACAG 332
DB 370 TGGAAAGACTACTATCTATAGTGAATGCTATAGTGAATGCTATAGTGAATGCTATAG 429
QY 333 GAGAGATTGCTGAGTCAAAAGAGCTGATTCCTTCTCTCCAGCATTTCTGTCC 392
DB 430 GAGAGGTTCTCCGAGTCAAGAGAGAGCTGAGAGCCCTCTCTCGAGCAGCTCCCTGGCC 489
QY 393 CAAGTTCCTGTGCTCGCTCCGAGAAACAATGATATCCGATACGCTTCTGAGAGAC 452
DB 490 ACCGTCCCTTCTGATCTCGGCAACAAGATGACATCCCTTACGCGCTGAGAGAG 549
QY 453 GAGTTCGCTTCAACTTGGGTTGACCA--TGACCACTGTTAAAGGAAAGGTAACCTG 509
DB 550 GAGCTCCGCTACCAACATGGGGCTGAGCACTTACCAACGCGCAAGGAGGAGGCTC 609
QY 510 GGAGATAGCAACATTCGCGCCCATTTGAGGTTTTCATGTGACGTAATTGCGCAAAATGGG 569
DB 610 GCGAGATCCCAAGCTTGGCCCCCTGAGAGGTTTCATGTGAGCATTCGCGCAAGATGGG 669
QY 570 TAGGTTGAAGGTTTCAAGTGAAGTGAACCACTACATCAAGT 609
DB 670 TATGGGATGGGTTCAAGTGGGTGTCACATACATCAAGT 709
RESULT 13
ADX45605
ID ADX45605 standard; cDNA; 986 BP.
XX
XX ADX45605;
XX
DT 21-APR-2005 (first entry)
XX
XX Plant full length insert polynucleotide seqid 20145.
XX
XX plant protectant; plant growth regulant; gene therapy; plant;
KM recombinant DNA construct; physical array; plant breeding marker;
KM cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KM extreme osmotic condition; pathogen tolerance; pest tolerance;
KM growth rate; cell cycle pathway; disease resistance;
KM galactomannan production; lignin production; plant growth regulator;
KM yield; plant growth; plant development; seed oil; protein yield;
KM protein content; gene; ss.
XX
XX Unidentified.
OS
XX US2004034888-A1.
PN
XX 19-FEB-2004.
XX
XX 28-APR-2003; 2003US-00425114.
PF
XX 06-MAY-1999; 99US-00304517.
PR 05-NOV-2001; 2001US-00985678.
XX
XX (LIU/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOV/) CAO Y.
XX
XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
PI

DR WPI; 2004-180133/17.

XX New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.

PS Claim 1; SEQ ID NO 20345; 15pp; English.

XX The invention describes a recombinant DNA construct comprising a
XX polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This sequence represents a plant full length insert
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.

XX Sequence 986 BP; 224 A; 250 C; 275 G; 237 T; 0 U; 0 Other;

XX Query Match 49.5%; Score 330.4; DB 13; Length 986;

XX Best Local Similarity 74.3%; Pred. No. 3.2e-103; Indels 3; Gaps 1;

XX Matches 431; Conservative 0; Mismatches 146; Indels 3; Gaps 1;

XX 33 ATGTTCTTGAAGTGGTTTACGCGTTCTTGCAGCATAGGGCTGTGCGAAGAGAG 92

XX 130 ATGTTCTTGAAGTGGTTTACGCGTTCTTGCAGCATAGGGCTGTGCGAAGAGAG 189

XX 93 GCCAAATCTGTTTCTGGGCTCTGCAATGCTGGCAAGACTCTTCTTGCACATGCTC 152

XX 190 GCCAAGATCTTCTTCTGCGCTCGACACGCGGCAAGACAGCTGCTCCATGCTC 249

XX 153 AAGGATGAGAACTGGGGCAACATCAACGAGATCAACGTCAGAGAGAGT 212

XX 250 AAGGACGAGGGTGTGACACACACCGACGACGACGAGCTGGAGAGCTTACG 309

XX 213 ATCAACAGATGAAATCAAGATTCGATCTGGGTGGCCACCAATCGCTCGACGCTG 272

XX 310 ATGGGCAAGATCAAGATTCGATCTGGGTGGCCACCAATCGCTCGACGCTG 369

XX 273 TGAAGGACTACTATGCTAAAGTGAATGCTATGCTTCTGTCAGCAATGACAG 332

XX 370 TGAAGGACTACTATGCTAAAGTGAATGCTATGCTTCTGTCAGCAATGACAG 429

XX 333 GAGGATTTCTGATCAAAAGAAAGAGCTGATCTTCTTCTCCGACGATCTCTGTC 392

XX 430 GAGGATTTCTGATCAAAAGAAAGAGCTGATCTTCTTCTCCGACGATCTCTGTC 489

XX 393 CAAGTCTCTGCTGCTCTGCGAAACAAGATGATATCCGATGCTTCTTCTGAAAG 452

XX 490 AATTTCTCATTTCTCATCTTCTGCAACAAGATGATATCCGATGCTTCTGAAAG 549

XX 453 GAGTGGGTTCACTTGGGTGACCA--TGACCACTGGTAAAGAAAGAGCTGACCTG 509

XX 550 GAGTGGGTTCACTTGGGTGACCA--TGACCACTGGTAAAGAAAGAGCTGACCTG 609

XX 510 GAGATGCAAACTGGGCCATGAGTTTCAATGCAATGAGTGGCCAAATGAGG 569

XX 610 GGGCACTCCAAATGTCGGCCACTTGAAGTTTCAATGCAATGAGTGGCCAAATGAGG 669

XX 570 TACGATGAAGTTTCAAGTGAATGACCAAGTCAATCAAGT 609

XX 670 TACGATGAAGTTTCAAGTGAATGACCAAGTCAATCAAGT 709

RESULT 14

ADX45551
ID ADX45551 standard; cDNA; 1051 BP.

XX ADX45551;

DT 21-APR-2005 (first entry)

XX Plant full length insert polynucleotide seqid 20291.

XX plant protectant; plant growth regulator; gene therapy; plant;
XX recombinant DNA construct; physical array; plant breeding marker;
XX cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
XX extreme osmotic condition; pathogen tolerance; pest tolerance;
XX growth rate; cell cycle pathway; disease resistance;
XX galactomannan production; lignin production; plant growth regulator;
XX yield; plant growth; plant development; seed oil; protein yield;
XX protein content; gene; ss.

XX Unidentified.

XX US2004034888-A1.

XX 19-FEB-2004.

XX 28-APR-2003; 2003US-00425114.

XX 06-MAY-1999; 99US-00304517.

XX 05-NOV-2001; 2001US-00985678.

XX (LIU/) LIU J.

XX (ZHOU/) ZHOU Y.

XX (KOVA/) KOVALIC D. K.

XX (SCRE/) SCREEN S. E.

XX (TABAS/) TABASKA J. E.

XX (CAOV/) CAO Y.

XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;

XX WPI; 2004-180133/17.

XX New recombinant DNA construct, useful for improving plant tolerance to

XX cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or

XX pests, for conferring increased resistance to plant disease, or for

XX improving yield.

XX Claim 1; SEQ ID NO 20291; 15pp; English.

XX The invention describes a recombinant DNA construct comprising a
XX polynucleotide consisting of a sequence encoding an amino acid sequence
XX available in electronic form from the US patent office at
XX ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
XX of the invention are also useful in physical arrays of molecules and as
XX plant breeding markers. The recombinant DNA construct is useful for
XX improving plant tolerance to cold, heat, drought, herbicides, extreme
XX osmotic conditions, pathogens or pests, for manipulating growth rate in
XX plant cells by modification of the cell cycle pathway, for conferring
XX increased resistance to plant disease, for producing galactomannan,
XX lignin or plant growth regulators, for increasing the rate of homologous
XX recombination in plants, for improving yield by modification of
XX photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
XX or by providing improved plant growth and development under at least one
XX stress condition or for modifying seed oil or protein yield and/or
XX content. This sequence represents a plant full length insert
XX polynucleotide that can be used in the recombinant DNA construct of the
XX invention.

XX Sequence 1051 BP; 236 A; 263 C; 291 G; 261 T; 0 U; 0 Other;

XX Query Match 49.5%; Score 330.4; DB 13; Length 1051;

XX Best Local Similarity 74.3%; Pred. No. 3.3e-103;

Matches 431; Conservative 0; Mismatches 146; Indels 3; Gaps 1;
QY 33 ATGTTCTTGTAGATGGTTTACGCGTTCTTTCGAGCATAGGGCTGTGGAGAGAG 92
DB 155 ATGTTCTTGTAGATGGTTTACGCGTTCTTTCGAGCATAGGGCTGTGGAGAGAG 214
QY 93 GCCAAAATCTGTTTCTGGGTTCTGCAAGATGCTGGCAAGACTCTTCTTGACATGCTC 152
DB 215 GCGAAGATCTCTTCTCTCGGCTCGACAAACGCGCAAGACACGCTGCTCCATGCTC 274
QY 153 AAGGATAGAAACCTGGGCAACATCAACCAACGAGATCCAAAGTCCAGAGAGAGT 212
DB 275 AAGGACAGCGGTTGTGACACACGACGACGACGACGACGACGACGACGACGACGAC 334
QY 213 ATCAACAGATGAAGTTCAAGATTCGATCTGGGTGGCCACACATCTGCTCGACGCTG 272
DB 335 ATCCGCAAGATCAAGTTCAAGGCTTCGACCTCGGCGGCAACGATTCGCGCGGCTC 394
QY 273 TGGAGGACTACTATGCTAAGTGAATGCTATGATGCTGCTGACGACGATAGACAG 332
DB 395 TGGAGGATTAAGTACGCAAGATGATGCTGATATACGCTGATAGATGATAG 454
QY 333 GAGAGATTTGCTGATCAAGAAAGAGCTGATCTCTCTCCGACGATCTCTCTCC 392
DB 455 GAGGATTTGCTGATCAAGAAAGAGCTGATCTCTCTCTCCGACGATCTCTCTCC 514
QY 393 CAAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 452
DB 515 AATGTTCCATTTCTCATCTCTGCGACAAAGATTAATCCGATATGCTGCTCTGAAAG 574
QY 453 GAGTTGCGGTTCACACTTGGGTTGACCA--TGACCACTGGTAAAGAACGTTGACCTG 509
DB 575 GAGTGGCGGTTCACACTTGGGTTGACCA--TGACCACTGGTAAAGAACGTTGACCTG 634
QY 510 GGAATAGCAACATTTGGGCTGATGAGTTTCAATGAGGATTTGAGCGAAATGGGG 569
DB 635 GGCACCTCCAAATGTCGGGCACTTGAAGTTTCAATGAGGATTTGAGCGAAATGGGG 694
QY 570 TACCGTGAAGGTTTCAAGTGAATGACCCAGATCAATCAAGT 609
DB 695 TACCGTGAAGGTTTCAAGTGAATGACCCAGATCAATCAAGT 734
RESULT 15
AD081658
ID AD081658 standard; cDNA; 1073 BP.
XX
AC AD081658;
XX
DT 21-APR-2005 (first entry)
XX
DE Plant full length insert polynucleotide seqid 378.
XX
KM plant protectant; plant growth regulant; gene therapy; plant;
KM recombinant DNA construct; physical array; plant breeding marker;
KM cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KM extreme osmotic condition; pathogen tolerance; pest tolerance;
KM growth rate; cell cycle pathway; disease resistance;
KM galactomannan production; lignin production; plant growth regulator;
KM yield; plant growth; plant development; seed oil; protein yield;
KM protein content; gene; ss.
XX
OS unidentified.
XX
PN US2004034888-A1.
XX
PD 19-FEB-2004.
XX
PF 28-APR-2003; 2003US-00425114.
XX
PR 06-MAY-1999; 99US-00304517.
XX
PR 05-NOV-2001; 2001US-00985678.
XX

PA (LIU/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TAB/) TABASKA J E.
PA (CAO/) CAO Y.
XX
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y,
XX WPI; 2004-180133/17.
XX
DR
XX
PT New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
PS Claim 1; SEQ ID NO 378; 15pp; English.
XX
XX The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?docid:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This sequence represents a plant full length insert
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.
XX
SQ Sequence 1073 BP; 242 A; 271 C; 294 G; 266 T; 0 U; 0 Other;
XX
Query Match 49.5%; Score 330.4; DB 13; Length 1073;
Best Local Similarity 74.3%; Pred. No. 3.3e-103;
Matches 431; Conservative 0; Mismatches 146; Indels 3; Gaps 1;
QY 33 ATGTTCTTGTAGATGGTTTACGCGTTCTTTCGAGCATAGGGCTGTGGAGAGAG 92
DB 177 ATGTTCTTGTAGATGGTTTACGCGTTCTTTCGAGCATAGGGCTGTGGAGAGAG 236
QY 93 GCCAAAATCTGTTTCTGGGTTCTGCAAGATGCTGGAAAGATCTTCTTGACATGCTC 152
DB 237 GCGAAGATCTCTTCTCTCGGCTCGACAAACGCGGCAAGACACGCTGCTCCATGCTC 296
QY 153 AAGGATAGAAACCTGGGCAACATCAACCAACGAGATCCAAAGTCCAGAGAGTGAAGT 212
DB 297 AAGGACAGCGGTTGTGACACACGACGACGACGACGACGACGACGACGACGACGAC 356
QY 213 ATCAACAGATGAAGTTCAAGATTCGATCTGGGTGGCCACACATCTGCTCGACGCTG 272
DB 357 ATCCGCAAGATCAAGTTCAAGGCTTCGACCTCGGCGGCAACGAGATTCGCGCGGCTC 416
QY 273 TGGAGGACTACTATGCTAAGTGAATGCTATGATGCTCTGACGACGAGTAGACAG 332
DB 417 TGGAGGATTAAGTCAAGGAGGTTGATGCTGATATCTGATGATGATGATGATGAT 476
QY 333 GAGGATTTGCTGATCAAGAAAGAGAGCTGATCTCTCTCCGACGATCTCTCTCC 392
DB 477 GAGGATTTGCTGATCAAGAAAGAGAGCTGATCTCTCTCCGACGATCTCTCTCC 536
QY 393 CAAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 452
DB 537 AATGTTCCATTTCTCATCTCTTGGCAACAAAGATTAATCCGATATGCTGCTCTGAAAG 596
QY 453 GAGTTGCGGTTCACACTTGGGTTGACCA--TGACCACTGGTAAAGAACGTTGACCTG 509

Db 597 GAGCTGCGGTATCACCCTAGGCTTAGCACTTCACAACCGGGAAGGCAAGTCAACCTT 656
QY 510 GGAGATAGCAACATTCGGGCCCATTTGAGGTTTCATGTGAGTATGTGCGCAAAATGGGG 569
Db 657 GGCGACTCCAAATGTCCGGCCACTTGAAGTTTCAATGCAAGTGTGTTCCCAAGATGGC 716
QY 570 TACGGTGAAGGTTTCAAGTGATGACCCAGTACATCAAGT 609
Db 717 TACGGCGATGTTCAAAGTGGTCTCCCAATACATCAAGT 756

Search completed: December 8, 2005, 23:08:48
Job time : 480 secs

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QY 365 TTCTCTCTCTCCGACGATTCCTGTCGCCAAGTTCCTGTCGTCCTGGGAAAACAAGAT 424
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 DB 275 CTCCTTGCTCTCGGATGAGCTCGCTCTCCCAAGTGCCTGCTGCTCTGGCAACAAGAT 216
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 DB 215 TGACATCCCTTACGCTCCCTCCAGATGATTCGCGTACACATCGCGCTGACATGAC 156
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 QY 485 CACTGTAAAGGAAGGATGACCTGGAGATAGCAATTCGGCCCATTTAGAGTTTTCAT 544
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 DB 95 GTGCAGTATTTGTCGCAAAATGGGCTTACGCGCAAGGTTTCAAGTGAATGACCGAGTATAT 36
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 QY 605 CAAGTATTTGTTTCTCTGTAAGAGGAACCTTA 637
 |||
 DB 35 TAAATGATTTGTTTGCATATAGACAAGAAAGTAA 3
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 RESULT 3
 BU609449/c 740 bp mRNA linear EST 22-OCT-2003
 LOCUS BU609449 normalized full length cDNA library, chloronemata,
 DEFINITION caulonemata and rhizoid-like protonemata Physcomitrella patens
 subsp. patens cDNA clone pphn47910 3', mRNA sequence.
 BU609449
 BU609449.1 GI:37851441
 EST.
 SOURCE Physcomitrella patens subsp. patens
 ORGANISM Physcomitrella patens subsp. patens
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
 Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
 1 (bases 1 to 740)
 Nishiyama,T., Fujita,T., Shin-I,T., Seki,M., Nishide,H.,
 Uchiyama,I., Kamiya,A., Carinci,P., Hayashizaki,Y., Shinozaki,K.,
 Kohara,Y. and Hasebe,M.
 Comparative genomics of Physcomitrella patens gametophytic
 transcriptome and Arabidopsis thaliana: implication for land plant
 evolution
 Proc. Natl. Acad. Sci. U.S.A. 100 (13), 8007-8012 (2003)
 12808149
 Contact: Tadasu Shin-I
 Center For Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshini@gene.nig.ac.jp
 A backbone of the vector is basically from pluescript II (KS),
 that was in vivo excised from a 1-F1C phage vector (Carinci et al.
 2001). 5' end of the cDNA that was digested with XhoI was ligated
 to SalI site of the vector and the 3' end including polyA tail was
 ligated to BamHI site of the
 vector(5'-gagagagagagatccacacctggagagatgttttttttttttttyn-3' was
 used as a 1st 3' primer, and
 5'-gggttcgagtcgacgtgttcgacacagcgatgactcgagacgannnn-3' as 2nd
 5'-hairpin primer, giving the following 5' boarder sequence,
 AGCCCAATCGCCGCGGCTGAATTCGTGAGACCG). cDNA insert could be
 amplified with conventional T7 and T3 primers. This full-length
 cDNA library was generated according to the method described in
 Nishiyama et al. (2003).
 Protonemata were blended by the POLYTRON, and then cultivated on
 the BCDAG medium for 13- 14 days under the continuous light.
 These clones are available from RIKEN Bio Resource Center
 (http://www.brc.riken.go.jp/lab/epd/Eng/index.html). The database
 of Physcomitrella EST clones is available at the PHYSCDBase
 (http://moss.nibb.ac.jp).
 Location/Qualifiers
 1..740
 /organism="Physcomitrella patens subsp. patens"
 /mol_type="mRNA"

ORIGIN
 Query Match 72.4%; Score 482.6; DB 3; Length 740;
 Best Local Similarity 85.2%; Pred. No.4e-134;
 Matches 539; Conservative 0; Mismatches 94; Indels 0; Gaps 0;
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 /db_xref="taxon:145481"
 /clone="pphn47910"
 /tissue_type="mixture of chloronemata, caulonemata and
 rhizoid-like protonemata"
 /clone_lib="normalized full length cDNA library,
 chloronemata, caulonemata and rhizoid-like protonemata"
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 |||
 DB 633 CGAGCCGAGATGTTTAAGCTCGATCATGTTATCGTAAATGGTTTATAGGCTTCT 574
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 QY 65 TCGAGCATAGGCGCTGTGCGAAGAGGCGCAAAATCTGTTTCTGGGCTCGACATGC 124
 |||
 DB 573 TCGAGCATAGGCTTGTGCGAAGAGGCGCAAAATCTGTTTCTGGGCTCGACATGC 514
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 QY 125 TGGCAAGTACTCTTTCGACATGCTCAAGATGAGAACTGGGGCAATCAACCAAC 184
 |||
 DB 513 CGGGAAGACACATTCGACATGCTCAAGATGAGAACTGGGGCAATCAACCAAC 454
 |||
 QY 185 GGAGTATCCAGCTCAGAGAGGATGATCAACAGAGTGAAGTTCAAGCATTCGATCT 244
 |||
 DB 453 GCAATATCCAACTCTGAAGATTTGACATCAATAGGTTGAAGTTCAAGCATTCGATCT 394
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 QY 245 GGGTGGCAACACATTCGTCGACGCGCTGTGAGGGCTACTATGCTTAAGTGAATCTAT 304
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 DB 393 AGGTGGTCAACGATGTCGACGTGTGAGGGGCTACTATGCTTAAGTGAATCTAT 334
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 QY 305 AGTGTATCTCTGACAGCATGACAGGAGATTTGCTGACTCAAGAAAGAGTCCG 364
 |||
 DB 333 CGTTTACCTTGTGACAGCATGACAGGAGAGGTTCTTGATCAAGAAAGAACTCGA 274
 |||
 QY 365 TTCTCTCTCTCCGACGATTCCTGTCGCCAAGTTCCTGTCGTCCTGGGAAAACAAGAT 424
 |||
 DB 273 CTCCTTGCTCTCGGATGAGCTCGCTCTCCCAAGTGCCTGCTGCTGGCAACAAGAT 214
 |||
 QY 425 TGAATATCCGATAGCGCTTCTTCTGAAGACGATTCGGTTTCACTTTGGTTGACCTGAC 484
 |||
 DB 213 TGACATCCCTTACGCTGCTCCGAAAGATGATTCGCGTACACATCGGCGCTGACATGAC 154
 |||
 QY 485 CACTGTAAAGGAAGGATGACCTGGAGATGACATTTGGCCCATTTAGAGTTTTCAT 544
 |||
 DB 153 CACTGTAAAGGAAGGATGACCTGGAGATGACATTTGGCCCATTTAGAGTTTTCAT 94
 |||
 QY 545 GTGCAGTATTTGTCGCAAAATGGGCTACGCTGAAGGTTTCAAGTGAATGACCCAGTACAT 604
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 DB 93 GTGCAGTATTTGTCGCAAAATGGGCTTACGCGCAAGGTTTCAAGTGAATGACCGAGTATAT 34
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 QY 605 CAAGTATTTGTTTCTCTGTAAGAGGAACCTTA 637
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 DB 35 TAAATGATTTGTTTGCATATAGACAAGAAAGTAA 1
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 RESULT 4
 BU599136/c 650 bp mRNA linear EST 22-OCT-2003
 LOCUS BU599136 normalized full length cDNA library, chloronemata,
 DEFINITION caulonemata and rhizoid-like protonemata Physcomitrella patens
 subsp. patens cDNA clone pphn25113 3', mRNA sequence.
 BU599136
 BU599136.1 GI:37841128
 EST.
 SOURCE Physcomitrella patens subsp. patens
 ORGANISM Physcomitrella patens subsp. patens
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
 Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
 1 (bases 1 to 650)
 Nishiyama,T., Fujita,T., Shin-I,T., Seki,M., Nishide,H.,

TITLE

Uchiyama, I., Kamiya, A., Carninci, P., Hayaishizaki, Y., Shinozaki, K., Kohata, Y. and Hasebe, M.
Comparative genomics of *Physcomitrella patens* gametophytic transcriptome and *Arabidopsis thaliana*: implication for land plant evolution

JOURNAL: Proc. Natl. Acad. Sci. U.S.A. 100 (13), 8007-8012 (2003)
PUBMED: 12808149
COMMENT: Contact: Tadasu Shin-i
Center for Genetic Resource Information
National Institute of Genetics
111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp

A backbone of the vector is basically from pBluescript II (KS), that was in vivo excised from a 1-FLC phase vector (Carninci et al., 2001). 5' end of the cDNA that was digested with XhoI was ligated to SalI site of the vector and the 3' end including polyA tail was ligated to BamHI site of the vector (5'-GAGAGAGAGATCCCAACCTTgagagagatTTTTTTTTTTTTTTVN-3' was used as a 1st 3' primer, and 5'-ggttcctgagtcgctgctgttccagacagcgatgactcgagacgcnnnnn-3' as 2nd 5'-hairpin primer, giving the following 5' boarder sequence. AGCCCAATCGCCGAGCTCGAATTCGTGAGAACG). cDNA insert could be amplified with conventional T7 and T3 primers. This full-length cDNA library was generated according to the method described in Uchiyama et al. (2003).
Protonemata were blended by the POLYTROX, and then cultivated on the BCDATG medium for 13-14 days under the continuous light. These clones are available from RIKEN Bio Resource Center (<http://www.brc.riken.go.jp/lab/epd/Eng/index.html>). The database of *Physcomitrella* EST clones is available at the PHYSCoBase (<http://mos.nibb.ac.jp/>).
Location/Qualifiers

1..650
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/mol_type="mRNA"
/db_spec="patens"
/db_xref="taxon:145481"
/clone="pPh16p22"
/tissue_type="mixture of chloronemata, caulonemata and rhizoid-like protonemata"
/clone_lib="normalized full length cDNA library,
chloronemata, caulonemata and rhizoid-like protonemata"

ORIGIN

Query Match 72.3%; Score 482.2; DB 3; Length 650;
Best Local Similarity 85.3%; Pred. No. 5.1e-134;
Matches 538; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

5 CGGGTCCGTAGATACCAAGCTGTGATCCATGTTCTTGTATGATTGTTTACGGCTTCT 64
631 CGAGCCGGCAATGTAAAGCTGTCATCATTTTATCTGATATGTTTATGCTTTCT 572
65 TGGCAGCATAGCGCTGTGCGAAGAGGCCAAATCTGTTTCTGGCTCTGCAAAATGC 124
571 TGGCAGCATAGCTTTGTGCGAAGAGGCCAAATCTGTTTCTGGCTCTGCAAAATGC 512
125 TGGCAGCATAGCTTTGTGCGAAGAGGCCAAATCTGTTTCTGGCTCTGCAAAATGC 184
511 CGGAGAGCGACACTTGTGCAATGCTCAAGATGAGAACTGGCGCAACATCAACCAAC 452
185 GCAGTATCAACGTCAGAGAGTGTGATCAACAGTGAAGTTCAAAGCATTCGATCT 244
451 GCAATATCAACATCTGAAAGATTGAGCATCAATAGGTGAAGTTCAAAGCATTCGATCT 392
245 GAGTGGCCACCAATTCGCTGACCGGTGTGAGAGGACATCTATGCTAAAGTGTGAT 304
391 AGGTGTGACACAGATGCTGACCGGTGTGAGAGGACATCTATGCTAAAGTGTGAT 332
305 AGTGTATCTGCTGACCGAGTGAACAGGAGAGATTTGCTAGTCAAAAGAGCTGCA 364
331 GGTTCACCTTGTGACCGAGTGAACAGGAGAGTTCCTGATCAAGAGAAAGATCTGA 272

QY 365 TTCTCTTCTCCGACGATTTCTGTCCCAAGTTCCTGTGCTCTCTCGGAAACAAGAT 424

DB 271 CTCCTGCTCTCCGAGATGATCGCTCTCCCAAGTTCCTGTGCTCTCTCGGAAACAAGAT 212

QY 425 TGAATCCGCTGACCTTCTTCTGAAGACGAGTGGGGTTCACACTTGGGTGACATGAC 484

DB 211 TGACATCCCTTACGCTGCTCCGAAATGATATGCGGTACACCTGAGCTTACCATGAC 152

QY 485 CACTGTAAAGAACCGGTGAACCTGAGATGCAACATTCGACCATTTGATTTTCAT 544

DB 151 CACTGTAAAGAACCGGTGAACCTGAGATGCAACATTCGACCATTTGATTTTCAT 92

QY 545 GTCCAGTATTTGCGCAAAATGGGGTACCGTGAAGTTTCAAGTGAATGCCATGAT 604

DB 91 GTCCAGTATTTGCGCAAAATGGGGTACCGTGAAGTTTCAAGTGAATGCCATGAT 32

QY 605 CAGGTATTTGTTTCTCTGTGAAGAGAACT 635

DB 31 TAAATATTTTGTGCAATGACAAAGAAAGT 1

RESULT 5
LOCUS B0952512/c 607 bp mRNA linear EST 14-JUN-2005

DEFINITION B0952512 pPh1 full-length cDNA library *Physcomitrella patens* subsp. *patens* cDNA clone pPh16p22 3', mRNA sequence.

ACCESSION B0952512 GI:67692279

VERSION B0952512.1

KEYWORDS EST.

SOURCE *Physcomitrella patens* subsp. *patens*

ORGANISM *Physcomitrella patens* subsp. *patens*

REFERENCE Fujita, T., Nishiyama, T., Shin-i, T., Kohata, Y. and Hasebe, M.

AUTHORS *Physcomitrella patens* subsp. *patens*

TITLE *Physcomitrella patens* subsp. *patens*

JOURNAL Unpublished (2005)

COMMENT Contact: Tadasu Shin-i
Center for Genetic Resource Information
National Institute of Genetics
111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp

Protonemata were inoculated on BCDATG medium for every ca. 5 days. Protoplasts were isolated from the protonemata, further incubated at 25°C under continuous light for 2-3 days. The regenerated cells, which were rich in cells at a stage during the first asymmetric cell division, were collected. Total RNA was extracted for constructing a full-length cDNA library. The database of the EST clones is available at the PHYSCoBase (<http://mos.nibb.ac.jp/>).
Location/Qualifiers

FEATURES

source

1..607
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/db_spec="patens"
/db_xref="taxon:145481"
/clone="pPh16p22"
/tissue_type="regenerated protoplasts (chloronemata)"
/dev_stage="at the first asymmetric cell division of protoplasts"
/clone_lib="pPh1 full-length cDNA library"
/note="Protonemata were inoculated on BCDATG medium for every ca. 5 days. Protoplasts were isolated from the protonemata, further incubated at 25°C under continuous light for 2-3 days. The regenerated cells, which were rich in cells at a stage during the first asymmetric cell division, were collected. Total RNA was extracted for constructing a full-length cDNA library."

ORIGIN

Query Match	71.1%: Score 474.2; DB 3; Length 607;
Best Local Similarity	86.3%: Pred. No. 1.3e-131;
Matches 524; Conservative 0; Mismatches 83; Indels 0; Gaps 0;	
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Qy 66	GCGAGCATAGGGCTGTGTGGCAGAGAGAGGCCAAAATCCTGTTTCTGGGCTTCGACATGCT 125
Db 547	GCGAGCATAGGTTGTGTGGCAGAGAGAGGCCAAAATCTTGTTCTGGGCTTCGACATGCTC 488
Qy 126	GGCAAGAATATCTCTTGTGCACATGCTGTAAGATGAGAACTGGGGCAATCAACCAAG 185
Db 487	GGGAAGACGAACTTCTGTGCACATGCTCAAGATGAGAACTGGGGCAATCAACCAAG 428
Qy 186	CAGTATCCAAACGTGCAGAGAGAGTGAATGATCAACAGAGTGAATTCAAAGCATTCGATCTG 245
Db 427	CAGTATCCAAACATTCGAAAGATTTAGCATCAATAGGGTGAAGTTCAAGCATTCGATCTA 368
Qy 246	GGTGGCCACACATATGCTCTGCAGCGCTGTGAGGGAATTAATGCTAAGTGGATGCTATTA 305
Db 367	GGTGTGACACAGATTTGCTGCAGCTGTGTGAGGGAATTAATGCTAAGTGGATGCTATTC 308
Qy 306	GTCGATCTCCGTCCGACCGAGTGAACAGGAGAGATTTGCTGATGCAAAAGAGCTGCAT 365
Db 307	GTTTAACTTGTTCGACGACGATTGACAAAGAGAGTTTCTGTAATCAAAAGAAATCTCAC 248
Qy 366	TCTCTTCTCTCCGACGATTTCTGTGCCAAGTTCCTGTGCTCGTCTCTGGAAACAAAGAT 425
Db 247	TCTTGTCTCTCGATGACTCGCTCTCCAAATGCTGTGTGCTGTGCTTGTGGCAACAGATT 188
Qy 426	GATATCCCGTACGGCTTCTTCTGAAGACGAGTTGGGTTCACACTTGGTTGACCATGACC 485
Db 187	GACATCCCTTACGCTGCTCTCCGAAGATGAATTTGGGTTACACACTGGCTGACATGACC 128
Qy 486	ACTGTGAAGAAAGCGGTGAACCTGTGGAGATAGCAACATTGGGCCATTTGAGTTTCAATG 545
Db 127	ACTGTGAAGAAAGAAAGCGGTGAACCTGAAGATAGCAACATTCGGCCATTTGAGTTTCAATG 68
Qy 546	TGCAGTATTGTGGCCAAAATGGGGGACGGTGAAGGTTCAAGTGGATGACCCAGTACATC 605
Db 67	TGCAGTATTGTGGCGTTAAGATGGGTTTACGGCGAAGGGTTCAAGTGGATGACCGAGTATT 8
Qy 606	AAGTAT 612
Db 7	AAATGAT 1
RESULT 6	
BU581125/c	502 bp mRNA linear EST 22-OCT-2003
LOCUS	BU581125 normalized full length cDNA library, chloronemata, calionemata and malformed buds Physcomitrella patens subsp. patens
DEFINITION	cDNA clone pnhb16k02.3, mRNA sequence.
ACCESSION	BU581125
VERSION	BU581125.1 GI:37823059
KEYWORDS	EST.
SOURCE	Physcomitrella patens subsp. patens
ORGANISM	Physcomitrella patens subsp. patens
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta; Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
AUTHORS	1 (bases 1 to 502) Nishiyama,T., Fujita,T., Shin-i,T., Seki,M., Nishide,H., Uchiyama,T., Kanuya,A., Carninci,P., Hayashizaki,Y., Shimozaki,K., Kohara,Y. and Haasebe,M. Comparative genomes of Physcomitrella patens gametophytic transcriptome and Arabidopsis thaliana: implication for land plant evolution Proc. Natl. Acad. Sci. U.S.A. 100 (13), 8007-8012 (2003) 12808149 JOURNAL PUBMED COMMENT Contact: Tadashi Shin-i Center For Genetic Resource Information

National Institute of Genetics
 111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshini@gene.nig.ac.jp
 A backbone of the vector is basically from pBluescript II (KS), that was in vivo excised from a 1-PstC phage vector (Carninci et al. 2001). 5' end of the cDNA that was digested with XhoI was ligated to SalI site of the vector and the 3' end including polyA tail was ligated to BamHI site of the vector (5'- GAGGAGAGAGATCGAACCCTGGAGAGATTTTTTTTTTTTTTTVN-3' was used as a 1st 3' primer, and 5'-gggttcgcagatgcgtgtccagacgcgcatgactgcgagaccgmnnn-3' as 2nd 5'-hairpin primer, giving the following 5' boarder sequence, AGGCCAAATCGCCGAGTCGATCGCAATCGCAACCG). cDNA insert could be amplified with conventional T7 and T3 primers. This full-length cDNA library was generated according to the method described in Nishiyama et al. (2003).
 Protonemata were blended by the POLYTRON, and then cultivated on the BCDARG medium for 13- 14 days under the continuous light. These clones are available from RIKEN Bio Resource Center (<http://www.brc.riken.go.jp/lab/epd/Eng/index.html>). The database of Physcomitrella EST clones is available at the PHYSCoBase (<http://mosa.nibb.ac.jp/>).
 Location/Qualifiers
 1..502

[illegible]

RESULT 7
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 LOCUS
 DEFINITION Bu607298 528 bp mRNA linear EST 22-OCT-2003
 Bu607298 normalized full length cDNA library, chloronemata, caulonemata and rhizoid-like protonemata Physcomitrella patens subsp. patens cDNA clone pphn39106 3', mRNA sequence.
 Bu607298
 Bu607298.1 GI:37849290
 EST.
 Physcomitrella patens subsp. patens
 Physcomitrella patens subsp. patens
 Bryophyta; Viridiplantae; Streptophyta; Embryophyta; Bryophyta; Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella. 1 (bases 1 to 528)
 Nishiyama, T., Fujita, T., Shin-i, T., Seki, M., Nishide, H., Uchiyama, I., Kamiya, A., Carninci, P., Hayashizaki, Y., Shinozaki, K., Kohara, Y. and Hasebe, M.
 Comparative genomes of Physcomitrella patens gametophytic transcriptome and Arabidopsis thaliana: implication for land plant evolution
 Proc. Natl. Acad. Sci. U.S.A. 100 (13), 8007-8012 (2003)
 12808149
 Contact: Tadao Shin-i
 Center for Genetic Resource Information
 National Institute of Genetics
 111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshini@genes.nig.ac.jp
 A backbone of the vector is basically from pBluescript II (KS), that was in vivo excised from a 1-FLC phase vector (Carninci et al. 2001). 5' end of the cDNA that was digested with XhoI was ligated to SalI site of the vector and the 3' end including polyA tail was ligated to BamHI site of the vector (5'-gagagagagagatccacacctgagagagttttttttttttt-3' was used as a 1st 3' primer, and 5'-gggttcgagatcgatcgctgttcacagacgagatcgagacgannnn-3' as 2nd 5'-hairpin primer, giving the following 5' boarder sequence, AGGCCAAATCGCCGAGCGAATTCGTCGAGAACGG). cDNA insert could be amplified with conventional T7 and T3 primers. This full-length cDNA library was generated according to the method described in Nishiyama et al. (2003).
 Protonemata were blended by the POLYTRON, and then cultivated on the BCDATG medium for 13-14 days under the continuous light. These clones are available from RIKEN Bio Resource Center (http://www.brc.riken.go.jp/lab/epd/Eng/index.html). The database of Physcomitrella EST clones is available at the PHSCODbase (http://mosr.nidb.ac.jp).
 Location/Qualifiers
 1..528
 /organism="Physcomitrella patens subsp. patens"
 /mol_type="mRNA"
 /sub_species="patens"
 /db_xref="taxon:145481"
 /clone="pphn39106"
 /issue_type="mixture of chloronemata, caulonemata and rhizoid-like protonemata"
 /clone_lib="normalized full length cDNA library, chloronemata, caulonemata and rhizoid-like protonemata"

ORIGIN
 Query Match 60.7%; Score 404.8; DB 3; Length 528;
 Best Local Similarity 85.4%; Pred. No. 1.2e-110;
 Matches 451; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

QY 110 GGGTTCGACATCGTGGCAAGACTACTTTCTGCATGCTCAAGATGAGAACTGGG 169
 DB 528 GGGCTTGCAGATGCGGGAGAGAGACACTTCTGCATGCTCAAGATGAGAACTGGG 469
 QY 170 GCAACATACCAACGCGATGTCACAGCTCGAGAGAGTTGGTATCAACAGATGAAGTT 229
 DB 468 GCAACATACCAACGCGATGTCACAGCTCGAGAGATGAGATGAGATGAGGTTGAAGTT 409

QY 230 CAAGCATTCGATCTGGTGGCCACAAATCGTCGACCGCTGTGGAGGACTACTATGCG 289
 DB 408 CAAGCATTCGATCTGAGTGTGTACACAGATGCTGCTGAGCTGTGTGAGGAGACTATATGC 349
 QY 290 TAAGGTGATGCTATAGTGTATCTCGTGCAGCAGATGACAGGAGAGATTTGCTAGTC 349
 DB 348 TAAGGTGATGCTATAGTGTATCTCGTGCAGCAGATGACAGGAGAGATTTGCTAGTC 289
 QY 350 AAAGAAAGACTGATCTCTCTCTCCGACGATTCCTGTGCCAAGTTCGTGCTGCTG 409
 DB 288 AAAGAAAGACTGATCTCTCTCTCCGACGATTCCTGTGCCAAGTTCGTGCTGCTG 229
 QY 410 CTGGGAAAACAAGATTGATATCCGTAACCTCTTCTTGAAGCAGATTGGGTTCAACT 469
 DB 228 CTTGGCAACAAGATTGATATCCCTTACCTGCTCCGAAAGATGATTGGGTTACACACT 169
 QY 470 TGGGTGACCATGACCACTGTGTAAGAACGCGTGAACCTGGAGATGACCAACTGGCC 529
 DB 168 CGGCTGACCATGACCACTGTGTAAGAACGCGTGAACCTGGAGATGACCAACTGGCC 109
 QY 530 CATTGAGTTTTCATGTGACGATATTTGTGCGCAAAATGGGGTACGCTGAAGGTTCAAGTG 589
 DB 108 CATTGAGTTTTCATGTGACGATATTTGTGCGTAAGATGCGTTACGGGAGGTTCAAGTG 49
 QY 590 GATGACCCAGTACATCAAGTATTTTCTGTGTAAGAGAACTTA 637
 DB 48 GATGACCCAGTACATCAAGTATTTTCTGTGTAAGAGAACTTA 1

RESULT 8
 BU173605/c
 LOCUS
 DEFINITION BU173605 full length cDNA library, chloronemata and young gametophores Physcomitrella patens subsp. patens cDNA clone pphn233, mRNA sequence.
 BU173605
 BU173605.1 GI:18341570
 EST.
 Physcomitrella patens subsp. patens
 Physcomitrella patens subsp. patens
 Bryophyta; Viridiplantae; Streptophyta; Embryophyta; Bryophyta; Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella. 1 (bases 1 to 638)
 Nishiyama, T., Fujita, T., Shin-i, T., Seki, M., Nishide, H., Uchiyama, I., Kamiya, A., Carninci, P., Hayashizaki, Y., Shinozaki, K., Kohara, Y. and Hasebe, M.
 Comparative genomes of Physcomitrella patens gametophytic transcriptome and Arabidopsis thaliana: implication for land plant evolution
 Proc. Natl. Acad. Sci. U.S.A. 100 (13), 8007-8012 (2003)
 12808149
 Contact: Tadao Shin-i
 Center for Genetic Resource Information
 National Institute of Genetics
 111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshini@genes.nig.ac.jp
 A backbone of the vector is basically from pBluescript II (KS), that was in vivo excised from a 1-FLC phase vector (Carninci et al. 2001). 5' end of the cDNA that was digested with XhoI was ligated to SalI site of the vector and the 3' end including polyA tail was ligated to BamHI site of the vector (5'-gagagagagatccacacctgagagagttttttttttttt-3' was used as a 1st 3' primer, and 5'-gggttcgagatcgatcgctgttcacagacgagatcgagacgannnn-3' as 2nd 5'-hairpin primer, giving the following 5' boarder sequence, AGGCCAAATCGCCGAGCGAATTCGTCGAGAACGG). cDNA insert could be amplified with conventional T7 and T3 primers. This full-length cDNA library was generated according to the method described in Nishiyama et al. (2003).
 Protonemata were blended by the POLYTRON, and then cultivated on

the BCDATG medium for 13-14 days under the continuous light. These clones are available from RIKEN Bio Resource Center (<http://www.brc.riken.go.jp/lab/epd/Eng/index.html>). The database of Physcomitrella EST clones is available at the PHYSCODbase (<http://moss.nibb.ac.jp>).

FEATURES

source

Location/Qualifiers
1. 638
/organism="Physcomitrella patens subsp. patens"
/mol_type="mRNA"
/sub_species="patens"
/db_xref="taxon:145481"
/clone="pPh3b23"
/issue_type="mixture of chloronemata and young gametophores with 2 to 5 leaves"
/clone_lib="full length cDNA library, chloronemata and young gametophores"

ORIGIN

Query Match 60.4%; Score 402.8; DB 3; Length 638;
Best Local Similarity 85.4%; Pred. No. 4.8e-110; Mismatches 77; Indels 0; Gaps 0;
Matches 449; Conservative 0; Mismatches 77; Indels 0; Gaps 0;
112 GTCTGCACATGCTGCGCAAGACTCTTCTGACATGCTCAAGATGAGAACTGGGCG 171
|||||
638 GTCTTGACATGCGGGAGAGACACTTCTGCATGCTCAAGATGAGAACTGGGCG 579
|||||
172 AACATCAACCAACGACGATATCCACCTCAGAGAGTTGATCAACAGAGTAAGTTCA 231
578 AACATCAACCAACGACGATATCCACCTCAGAGAGTTGATCAACATAGGGTGAAGTTCA 519
232 AAGCATTCATCTGGGTGGCGACACAAATGCTGACGCGGTGAGAGGACTATATGCTA 291
518 AAGCATTCATCTGGGTGGCGACACAAATGCTGACGCGGTGAGAGGACTATATGCTA 459
292 AGGTGATGCTATAGTATCTCTGTCGACGACATAGACAGAGAGATTTGCTGATCA 351
458 AGGTGATGCTATAGTATCTCTGTCGACGACATAGACAGAGAGATTTGCTGATCA 399
352 AGAAGAGCTCGATCTCTCTCGACGATTTCTGTCACAGTTCTCTGTCGTC 411
398 AGAAGAGCTCGATCTCTCTCGACGATTTCTGTCACAGTTCTCTGTCGTC 339
412 TGGGAAACAAGATGATATCCCTAGCGCTTCTTGAAGCGAGTGGCGTTCACTTG 471
338 TGGGAAACAAGATGATATCCCTAGCGCTTCTTGAAGCGAGTGGCGTTCACTTG 279
472 GGTGACCATGACCACTGTTAAGAAACGCTGAACCTGGAGATAGCAATTCGGCCCA 531
278 GGTGACCATGACCACTGTTAAGAAACGCTGAACCTGGAGATAGCAATTCGGCCCA 219
532 TTGAGGTTTTCATGTCAGATATTGTGGCAAAATGGGGTACGGTGAAGTTTCAAGTGA 591
218 TTGAGGTTTTCATGTCAGATATTGTGGCAAAATGGGGTACGGTGAAGTTTCAAGTGA 159
592 TGACCCAGTACATCAAGTATTTTCTCTGTAAGAGAGAACTTA 637
158 TGACCCAGTACATCAAGTATTTTCTCTGTAAGAGAGAACTTA 113

RESULT 9

BU171787/c

LOCUS

DEFINITION

BU171787 full length cDNA library, chloronemata and young gametophores Physcomitrella patens subsp. patens cDNA clone pPh30c04 3', mRNA sequence.

VERSION

BU171787.1 GI:18339760

KEYWORDS

SOURCE

ORGANISM

Physcomitrella patens subsp. patens
Physcomitrella patens subsp. patens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta; Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella;
1 (bases 1 to 567)

AUTHORS

TITLE

JOURNAL

PUBMED
12808149

COMMENT

Nishiyama, T., Fujita, T., Shin-i, T., Seki, M., Nishide, H., Uchiyama, I., Kamiya, A., Carninci, P., Hayashizaki, Y., Shinozaki, K., Kohara, Y., and Hasebe, M.
Comparative genomics of Physcomitrella patens gametophytic transcriptome and Arabidopsis thaliana: implication for land plant evolution
Proc. Natl. Acad. Sci. U.S.A. 100 (13), 8007-8012 (2003)
Contact: Tadao Shin-i
Center for Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp
A backbone of the vector is basically from pBluescript II (KS), that was in vivo excised from a 1-FLC phase vector (Carninci et al. 2001). 5' end of the cDNA that was digested with XhoI was ligated to SalI site of the vector and the 3' end including polyA tail was ligated to BamHI site of the vector (5'-gagagagagagatccacccttgagaggtttttttttttttt-3' was used as a 1st 3' primer, and 5'-ggttctcgagtcagtcgtgttccagacagcgatgactcgagAACGNNNN-3' as 2nd 5'-hairpin primer, giving the following 5' boarder sequence, AGGCCAATGCGCGAGCTCGAATTCGCGAAGCCG). cDNA insert could be amplified with conventional T7 and T3 primers. This full-length cDNA library was generated according to the method described in Nishiyama et al. (2003).
Protonemata were blended by the POLYTRON, and then cultivated on the BCDATG medium for 13-14 days under the continuous light. These clones are available from RIKEN Bio Resource Center (<http://www.brc.riken.go.jp/lab/epd/Eng/index.html>). The database of Physcomitrella EST clones is available at the PHYSCODbase (<http://moss.nibb.ac.jp>).

FEATURES

source

Location/Qualifiers
1. 567
/organism="Physcomitrella patens subsp. patens"
/mol_type="mRNA"
/sub_species="patens"
/db_xref="taxon:145481"
/clone="pPh30c04"
/issue_type="mixture of chloronemata and young gametophores with 2 to 5 leaves"
/clone_lib="full length cDNA library, chloronemata and young gametophores"

ORIGIN

Query Match 60.2%; Score 401.4; DB 3; Length 567;
Best Local Similarity 85.0%; Pred. No. 1.2e-109; Mismatches 79; Indels 0; Gaps 0;
Matches 447; Conservative 0; Mismatches 79; Indels 0; Gaps 0;
112 GTCTGCACATGCTGCGCAAGACTCTTCTGACATGCTCAAGATGAGAACTGGGCG 171
|||||
567 GTCTTGACATGCGGGAGAGACACTTCTGCATGCTCAAGATGAGAACTGGGCG 508
|||||
172 AACATCAACCAACGACGATATCCACCTCAGAGAGTTGATCAACAGAGTAAGTTCA 231
507 AACATCAACCAACGACGATATCCACCTCAGAGAGTTGATCAACATAGGGTGAAGTTCA 448
232 AAGCATTCATCTGGGTGGCGACACAAATGCTGACGCGGTGAGAGGACTATATGCTA 291
447 AAGCATTCATCTGGGTGGCGACACAAATGCTGACGCGGTGAGAGGACTATATGCTA 388
292 AGGTGATGCTATAGTATCTCTGTCGACGACATAGACAGAGAGATTTGCTGATCA 351
387 AGGTGATGCTATAGTATCTCTGTCGACGACATAGACAGAGAGATTTGCTGATCA 328
352 AGAAGAGCTCGATCTCTCTCGACGATTTCTGTCACAGTTCTCTGTCGTC 411
327 AGAAGAGCTCGATCTCTCTCGACGATTTCTGTCACAGTTCTCTGTCGTC 268
412 TGGGAAACAAGATGATATCCCTAGCGCTTCTTGAAGCGAGTGGCGTTCACTTG 471
|||||

D _b	267 TTGGCAACAAAGATTGACATCCCTTAAGCTGCCTCGAAGAATGAATTTGGGTACAACACTGG	208
Q _y	472 GGTTGACCATGACCACTGCTGTAAAGAACGGTGAACCTTGGAGATTCACAACATTGGGCCCA	531
D _b	207 GCCTGACCATGATACCACTGGCAAAGGAAACGGTAGAACTGTAMAGGATATGGCAATCCGGCCCCA	148
Q _y	532 TTGAGTTTTTCATGTGCAGTATTGTGCGCAAAATGGGGTACGGGTGAAGSTTTCAAGTTGA	591
D _b	147 NTGAGTTTTTCATGTGCAGTATGAGCCTAAGATGGGTTACGGCCAAAGGGTTCAAGTGA	88
Q _y	592 TGACCCAGTACATCAAGTATTTGTTTTCTGTGAAGAAGAACTTA	637
D _b	87 TGAAGCAGTATTTTAAATGATTTGTTGCAATGACAGAAAGTAA	42

RESULT 10	
LOCUS	CN206979
DEFINITION	CN206979 861 bp mRNA linear EST 30-APR-2006 Tort739 Gemetophyte rehydration Library Tortula ruralis cDNA, mRNA Sequence.
ACCESSION	CN206979
VERSION	CN206979.1
KEYWORDS	GI:46903710
SOURCE	EST.
ORGANISM	Tortula ruralis Tortula ruralis Tortula ruralis

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
PUBMED

1 (bases 1 to 861)
Oliver, M. J., Dowd, S. E., Zaragosa, J., Marget, S. A. and Payton, P. R.
The rehydration transcriptome of the desiccation-tolerant bryophyte
Tortula ruralis: transcript classification and analysis
BMC Genomics 5 (1), 89 (2004)
15546486
Contact: Oliver Melvin J

3810 4th St, Lubbock, TX 79415, USA
Tel.: 806-749-5560
Fax: 806-723-5272
Email: moliver@lbk.ars.usda.gov
PCR Primers
FORWARD: GTTTCGACGTCACGAC
BACKWARD: CAGGAACGCTGTGAC.
Location/Qualifiers
1. 861
/organism="Tortula ruralis"
/mol_type="mRNA"
/db_xref="taxon:38588"
/clone_lib="Gametophyte rehydration library"
/note="Organ: Green Gametophyte; Vector: pSport1; Site_1:
Sail; Site_2: NotI"

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Matches 487; Conservative 0; Mismatches 121; Indels 2; Gaps 2				
QY	25	CTGCTACCATGTTCTTGTAATGCTTTTACGCGCTTTCGCGAGCATAGGCTGTGGC	84	
Db	164	CTACACACCATGTTCTCGTGAATGTTCTTAGGGCTCTTGCCAGCATAGGGCTGTGGC	223	
QY	85	AGAGGAGAGCCAAATCTGTTTCTGGGCTTCGAAATCTGGCAAGCTACTCTTTCGC	144	
Db	224	AGAAAGAGGCCAAATCTCTTCTTGGGCTTCGAAACGCGGCAAGACACGCTCTTC	283	
QY	145	ACATGCTCAAGATGAGAACTGGGGCAATCAACCAAGCATATCCAACTGCAGAG	204	
Db	284	ACATGCTCAAGATGAGAAATTGGGGCAGCATCAACCAAGCATATCCCACTTGCAGAG	343	
QY	205	AGTTGAGTATCAACAGAGTGAAGTTCAAAGCATTCGATCTGGGTGGCAACACATCGCTC	264	
Db	344	AGCTGAGATCAACAGAGTGAAGTTCAAAGCTTTGATTTGGGGGGGCAACCTATCGCA	403	

QY	265	GAGCGGTGGAGGAACTACTATGCTAAAGTGGATGCTATAGTGTATCTGTCGACGACG	324
Db	404	GCGGTGTGGAGAGACTATTATGCCAAGGTGGATGCCATAGTCTACTGCTGGACGCC	463
QY	325	TAGACAGGAGAGATTGTGCTAGTCCAAAGAAAGCTCGATTCTTCTCTCGACGATT	384
Db	464	TAGACAAAGAGAGATTCCAGAGTCCGAAAGAAAGAGCTGACTCGTTCTCTCAGACGACA	523
QY	385	CTCTGTCCCAAGTTTCTGTGCTGCTCTGGGAAACCAAGATTGATATCCGTAAGCTTCTT	444
Db	524	CTCTCTCCCAAGTTTCTGTGCTGCTGCTGGGAAACCAAGATTGACATCCGTAATGCGGCT	583
QY	445	CTGAAAGCGAGTTGCGGTTCCACTTGGGTTGACCATGACCACTGGTAAAGAAAGCGTGA	504
Db	584	CTGAGAGAGAGCTCGGCTATTCCCTGGGCTGACCATGACCAAGGCCATGGAGCGGTGA	643
QY	505	ACCTGGAGAGATAGCAATTCGGGCCCATTTAGGTTTTCATGTGCAAGTATTTGGCGCAAA	564
Db	644	ACCTGGGCGACAGCAATTCGGGCCCATTCGAGGCTTTCATGTGCAAGTATTTGGCGAAGA	703
QY	565	TGGGGTACGGTGAAGGTTTCAGTGGATGACCCAGTACATCAAGTGAATTTGTTTCTGTG	624
Db	704	TGGGTTGGGAGAACG-GTCACTGGATTAACGC-GTACATCAGTTGATGATAGTATTGCT	761
QY	625	AAAGAGGAAC	634
Db	762	CATGTAGAAC	771

RESULT 11	LOCUS	600 bp	RNA	linear	EST 22-OCT-2003
BU595842/c	LOCUS	600 bp	RNA	linear	EST 22-OCT-2003
DEFINITION	BU595842	normalized full length cDNA library, chloronemeta, BU595842			
		chloronemeta and rhizoid-like protonemata Physcomitrella patens			
		subsp. patens cDNA clone phn10e13 3', mRNA sequence.			

ACCESSION	BJ595842	
VERSION	BJ595842.1	GI:37637834
KEYWORDS	EST.	
SOURCE	Physcomitrella patens subsp. patens	
ORGANISM	Physcomitrella patens subsp. patens	

REFERENCE	AUTHORS	TITLE	JOURNAL	PUBMED	COMMENT
1 (bases 1 to 600)	Nishiyama, T., Fujita, T., Shin-i, T., Seki, M., Nishide, H., Uchiyama, I., Kamiya, A., Carninci, P., Hayashizaki, Y., Shinozaki, K., Kohara, Y. and Hasebe, M.	Comparative genomics of <i>Physcomitrella patens</i> gametophytic transcriptome and <i>Arabidopsis thaliana</i> : implication for land plant evolution	Proc. Natl. Acad. Sci. U.S.A. 100 (13), 8007-8012 (2003)	12808149	Contact: Tadaasu Shin-i

Center For Genetic Resource Information
National Institute of Genetics
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Tel.: 81-559-81-6856
Fax: 81-559-81-6855
Email: tsuhid@genes.nig.ac.jp
A backbone of the vector is basically from pBluescript II (Ks),
that was in vivo excised from a 1-FIC phage vector (Carlini et al.,
2001). 5' end of the cDNA that was digested with XhoI was ligated
to SalI site of the vector and the 3' end including polyA tail was
ligated to BamH site of the
vector(5'- gagagagagagatcacaacccctgagagatTTTTTTTTTTTTTTVN-3' was
used as a 1st 3' primer, and
5'-gggttcgcgcatcgcgtgtccacagcagatgactcagacacgannnn-3' as 2nd
5'-hairpin primer, giving the following 5' boarder sequence,
AGGCCAAATCGCCGCGCTCGAATTGTCGAGACCG). cDNA insert could be
amplified with conventional T7 and T3 primers. This full-length
cDNA library was generated according to the method described in
Nishiyama et al. (2003).
Protonemata were blended by the POLYTRON, and then cultivated on
the BCDAG medium for 13- 14 days under the continuous light.

QY 524 TCGGCCATTGAGTTTTCATGTCAGTATTTGCGCAAAATGGGGTACGTTAAGTTT 583
 Db 205 CCGGCCATTGAGTTTTCATGTCAGTATTTGCGCAAAATGGGGTACGTTAAGTTT 146
 QY 584 CAAGTGATGATGACCAATGATCATCAAGTATTTTCTGTGAAAGAGAACTTA 637
 Db 145 CAAGTGATGATGACCAATGATCATCAAGTATTTTCTGTGAAAGAGAACTTA 92
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 B9941869 684 bp mRNA linear EST 13-JUN-2005
 LOCUS B9941869 phpf.full-length cDNA library Physcomitrella patens subsp.
 DEFINITION patens cDNA clone phpf16p22 5', mRNA sequence.
 ACCESSION B9941869
 VERSION B9941869.1 GI:67569045
 KEYWORDS EST.
 SOURCE Physcomitrella patens subsp. patens
 ORGANISM Physcomitrella patens subsp. patens
 Eukaryota; Viridiplantae; Streptophyta; Bryophyta;
 Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
 1 (bases 1 to 684)
 Fujita, T., Nishiyama, T., Shin-i, T., Kohara, Y. and Hasebe, M.
 Physcomitrella patens EST at a stage of the first asymmetric cell
 division of protoplasts
 Unpublished (2005)
 JOURNAL Contact: Tadashi Shin-i
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshin@genes.nig.ac.jp
 Protoplasts were inoculated on BGDANG medium for every ca. 5 days.
 Protoplasts were isolated from the protoplasts, further incubated
 at 25C under continuous light for 2-3 days. The regenerated cells,
 which were rich in cells at a stage during the first asymmetric
 cell division, were collected. Total RNA was extracted for
 constructing a full-length cDNA library. The database of the EST
 clones is available at the PHYSCDBase (http://moss.nibb.ac.jp).
 FEATURES
 source
 location/Qualifiers
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 /mol_type="mRNA"
 /sub_species="patens"
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 /clone="phpf16p22"
 /tissue_type="regenerated protoplasts (chloronemata)"
 /dev_stage="at the first asymmetric cell division of
 protoplasts"
 /clone_lib="pphf full-length cDNA library"
 /note="Protoplasts were inoculated on BGDANG medium for
 every ca. 5 days. Protoplasts were isolated from the
 protoplasts, further incubated at 25C under continuous
 light for 2-3 days. The regenerated cells, which were rich
 in cells at a stage during the first asymmetric cell
 division, were collected. Total RNA was extracted for
 constructing a full-length cDNA library."
 ORIGIN
 Query Match 51.8%; Score 345.8; DB 3; Length 684;
 Best Local Similarity 86.1%; Pred. No. 8.1e-93;
 Matches 383; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
 QY 5 CGGTCCTGATAGTACCAAGCTGTGATTTCTTTAGATTTGATTTTACGGCTTTCT 64
 Db 240 CGAGCCCGGACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 299
 QY 65 TGGCAGCATAGGCGTGTGGCAAGAGGCAAAATCTGTTCTGGGTCGCAATGTC 124
 Db 300 TGGCAGCATAGGCGTGTGGCAAGAGGCAAAATCTGTTCTGGGTCGCAATGTC 359

QY 125 TGGCAAGACTACTCTTTCTGCAATGCTCAAGATGAGAAATCGGGCAACATCAACAC 184
 Db 360 CGGAGAGACACATCTCTCACATGCTCAAGATGAGAAATCGGGCAACATCAACAC 419
 QY 185 GCAGTATCCAGGTGAGAGAGTGTGATGATCAACAGATGAGAGTGTGAGATGATGAT 244
 Db 420 GCAGTATCCAGGTGAGAGAGTGTGATGATCAACAGATGAGAGTGTGAGATGATGAT 479
 QY 245 GGGTGGCAACAAATGCTGACGCGTGTGAGAGGACTATATGCTTAAGTGTGAT 304
 Db 480 AGGTGTGACACGATTTGCTGACGCTGTGTGAGAGGACTATATGCTTAAGTGTGAT 539
 QY 305 AGTGTATCTGCTGACAGGATGACAGGAGAGATTTGCTGACTCAAAAGAGTGTG 364
 Db 540 CGTTTACCTTGTGACAGGATGACAGGAGAGTGTGCTGATCAAAAGAGTGTG 599
 QY 365 TTCTTCTCTGCGAGATTTCTGTGCCAAGTCTGTGCTGTGCTGTGCTGTGCTGTG 424
 Db 600 CTCTTCTCTGCGAGATTTCTGTGCCAAGTCTGTGCTGTGCTGTGCTGTGCTGTG 659
 QY 425 TGATATCCGTAAGCTTCTTGTGAA 449
 Db 660 TGACATCCCTTAAGCTGCTCGAA 684
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 LOCUS pam01-5m61-b07 Persea americana cDNA clone pam01-5m61-b07 5',
 mRNA sequence.
 ACCESSION CK748609
 VERSION CK748609.1 GI:42639032
 KEYWORDS EST.
 SOURCE Persea americana (avocado)
 ORGANISM Persea americana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; magnoliids; Laurales; Lauraceae;
 Persea.
 1 (bases 1 to 751)
 dePamphilis, C., Carlson, J., Ma, H., Solitis, D., Solitis, P.,
 Oppenheimer, D., Frohlich, M., Doyle, J., Tanksey, S., Webb, M.,
 Leebens-Mack, J., Landherr, L., Ilut, D. and Wall, K.
 Generation of ESTs from early flower buds of Persea americana
 Unpublished (2003)
 JOURNAL Contact: Claude dePamphilis or James Leebens-Mack
 COMMENT Mueller Laboratory
 Penn State University
 208 Mueller Laboratory, Department of Biology, ATTN Rm212, Penn
 State University, University Park, PA 16802, USA
 Tel: 814 863 6431
 Fax: 814 865 9131
 Email: cwdi@psu.edu or jhl10@psu.edu
 The sequence provided is trimmed of vector and low quality regions.
 Full sequence and original trace file are available from the Plant
 Genome Network website (http://pgn.cornell.edu)
 Plate: pam01-5m61 row: b column: 07
 Seq primer: M13P.
 FEATURES
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 Site 2: XhoI. This is a directionally cloned,
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 the Floral Genome Project (FGP). The Floral Genome Project
 is funded by NSF's Plant Genome Research Program

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US-09-828-310-1/c
; Sequence 1, Application US/09828310
; Patent No. 6689939
; GENERAL INFORMATION:
; APPLICANT: COSTA E SILVA, OSMALDO DA
; APPLICANT: BOMBERT, HANS J.
; APPLICANT: VAN THIELEN, NOCHA
; APPLICANT: CHEN, ROUYING
; TITLE OF INVENTION: GTP BINDING STRESS-RELATED PROTEINS AND METHODS OF USE
; TITLE OF INVENTION: IN PLANTS
; FILE REFERENCE: 16313-0039
; CURRENT APPLICATION NUMBER: US/09/828,310
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/196,001
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 805
; TYPE: DNA
; ORGANISM: Physcomitrella patens
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QY 125 TGGCAAGACTATCTTTCTGCATGCTCAAGATGAGAAACTGCGGCAACATCAACCAAC 184
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Db 661 TGGCAAGACTATCTTTCTGCATGCTCAAGATGAGAAACTGCGGCAACATCAACCAAC 602
QY 185 GCAATATTCACACGTCAGAGAGGTGAGTATCAACAGAGTAAGTTCAAAGATTCGATCT 244
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Db 481 AGTGTATCTCTGTCGACGACGATGACAGAGAGAGATTTCGTGAGTCAAGAAAGAGCTGA 422
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RESULT 3
US-09-270-767-13105
; Sequence 13105, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13105
; LENGTH: 3191
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-13105
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Best Local Similarity 61.8%; Pred. No. 1.7e-67;
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QY 273 TGGAGGACTACTATGCTAAGGTGATGCTATAGTATCTCGTCGACGACGATGACAG 312
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Db 414 TGGAGGACTACTTCCCTGCTGTGACGCGCATGTTTCTTAATTAACGCTGGACCG 473
QY 333 GAGAGATTTGCTGATCAAGAAAGAGCTCGATTTCTTCTCTCGACGATTCCTGTC 392
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RESULT 4

US-09-533-559-6998
; Sequence 6998, Application US/09533559
; Patent No. 6902887
; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rey
; APPLICANT: Jeffrey R. Shuster
; APPLICANT: Sakari Kauppinen
; APPLICANT: Ib Groth Clausen
; APPLICANT: Peter Bjarke Olsen
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: Expression
; FILE REFERENCE: 5849.200-US
; CURRENT APPLICATION NUMBER: US/09/533,559
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 09/273,623
; EARLIER FILING DATE: 1999-03-22
; NUMBER OF SEQ. ID NOS: 7860
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ. ID NO 6998
; LENGTH: 716
; TYPE: DNA
; ORGANISM: Aspergillus oryzae
US-09-533-559-6998

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RESULT 5

US-08-825-780-2
; Sequence 2, Application US/08825780
; Patent No. 5834238
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: NOVEL HUMAN GTP BINDING P
; TITLE OF INVENTION: ROTHEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/825,780
; FILING DATE: Filed Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0264 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ. ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 724 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BESTTUT14
; CLONE: 2742252
US-08-825-780-2

Query Match 26.9%; Score 179.2; DB 2; Length 724;
Best Local Similarity 58.5%; Pred. No. 1.8e-54;
Matches 332; Conservative 0; Mismatches 233; Indels 3; Gaps 1;

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; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
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; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
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; EARLIER APPLICATION NUMBER: 60/038,621
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; EARLIER APPLICATION NUMBER: 60/056,662

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; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
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; EARLIER APPLICATION NUMBER: 60/056,877
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 / EARLIER APPLICATION NUMBER: 60/056,908
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 / EARLIER APPLICATION NUMBER: 60/048,964
 / EARLIER FILING DATE: 1997-06-06
 / EARLIER APPLICATION NUMBER: 60/057,650
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 / EARLIER APPLICATION NUMBER: 60/056,884
 / EARLIER FILING DATE: 1997-08-22
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 / EARLIER FILING DATE: 1997-09-05
 / EARLIER APPLICATION NUMBER: 60/049,610
 / EARLIER FILING DATE: 1997-06-13
 / EARLIER APPLICATION NUMBER: 60/061,060
 / EARLIER FILING DATE: 1997-10-02

Query Match 26.9%; Score 179.2; DB 3; Length 1228;
 Best Local Similarity 58.5%; Pred. No. 2.5e-54;
 Matches 332; Conservative 0; Mismatches 233; Indels 3; Gaps 1;

QY 47 TTGGTTTACGGCTTCTTCGAGCATAGGGCTGTGCGAAGAGGCCCAATCCTGTT 106
 DB 118 TGGTTTACGACAGTGTCTTCACTTTTATAGATTATATAGAAACCTGTAACTGGTATT 177
 QY 107 TCTGGTCTCGAATGCTGCGAAGCTACTTCTTGCACATGCTCAGAGATGAGAACT 166
 DB 178 TCTGGATTGATTAATGACAGAAAAACAATGCTACACATGCTAAAGATGACAGACT 237
 QY 167 GGGGCAACATCAACCAACCATATCCACGTCAGAGAGTTGATATCAACAGATGAA 226
 DB 238 TGGACAAACATGTCACCACTTACATCCCTTCCAGAACTGACCATGCTGCTATGAC 297
 QY 227 GTTCAAGCATTCGATCTGCTGGTGGCCACACAATCGCTGACCGTGTGAGGGAGCTACTA 286
 DB 298 GTTACACATTTTGTATCTGGTGTGACATGTTCAAGCTGCAAGAGTGTGAAAAAAGTAACT 357
 QY 287 TGTAAAGTGATGCTATAGTATCTGTCAGCAGATGAGCAAGGAGAGATTGCTGTA 346
 DB 358 TCTGTATCAATATGAGCATTTGATTTCTGTGATGTCAGACACAGAAAGCTGTAGA 417
 QY 347 GTCAAGAAAGAGCTGATTTCTTCTCCGACGATTTCTGTCCAGTTCTCTGCT 406
 DB 418 GTCAAAAGAAAGACTGATTCATATGACATGATGAAACCATGCTTAATGTGCTTAACT 477
 QY 407 CGTCCGGGAAACAAGATTGATATCCGTAAGCTTCTTGAAGACGATGCGGTTCA 466
 DB 478 GATTTTGGAAATATGATGACAGACCTTGAAGCATCAGTAAAGAGGTTGGAGAGAT 537
 QY 467 ACTTGGGTT---GACCATGACCACTGTGTAAAGAAAGTGAACCTGGAGATAGCAACAT 523
 DB 538 GTTGTGTTATATGTCAGACAACAGAAAGGAGTATATCTGTAAAGAACTGAATGC 597
 QY 524 TGGGCCATTAAGGTTTATGTCAGATTTGTGCGCAAAATGGGGTACGGTGAAGTTT 583
 DB 598 CCGACCTTAAGAAAGTTTATGTCAGATTTGTGTCACAAAGAAAGAGTTTACGAGAAAGCTT 657
 QY 584 CAAAGTGATGACCCGATACATCAAGTGA 611
 DB 658 CCGCTGATGACGACGATACATTTGATTAA 685

RESULT 7
 US-09-149-476-146
 ; Sequence 146, Application US/09149476
 ; Patent No. 6420526
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: 186 Human Secreted proteins

[illegible]

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/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,590
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,594
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,589
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,593
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,614
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/043,578
/ EARLIER FILING DATE: 1997-04-11
/ EARLIER APPLICATION NUMBER: 60/043,576
/ EARLIER FILING DATE: 1997-04-11
/ EARLIER APPLICATION NUMBER: 60/047,501
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/043,670
/ EARLIER FILING DATE: 1997-04-11
/ EARLIER APPLICATION NUMBER: 60/056,632
/ EARLIER FILING DATE: 1997-08-22
/ EARLIER APPLICATION NUMBER: 60/056,664
/ EARLIER FILING DATE: 1997-08-22
/ EARLIER APPLICATION NUMBER: 60/056,876
/ EARLIER FILING DATE: 1997-08-22
/ EARLIER APPLICATION NUMBER: 60/056,881
/ EARLIER FILING DATE: 1997-08-22
/ EARLIER APPLICATION NUMBER: 60/056,909
/ EARLIER FILING DATE: 1997-08-22
/ EARLIER APPLICATION NUMBER: 60/056,875
/ EARLIER FILING DATE: 1997-08-22
/ EARLIER APPLICATION NUMBER: 60/056,862
/ EARLIER FILING DATE: 1997-08-22
/ EARLIER APPLICATION NUMBER: 60/056,887
/ EARLIER FILING DATE: 1997-08-22
/ EARLIER APPLICATION NUMBER: 60/056,908
/ EARLIER FILING DATE: 1997-08-22
/ EARLIER APPLICATION NUMBER: 60/048,964
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/057,650
/ EARLIER FILING DATE: 1997-09-05
/ EARLIER APPLICATION NUMBER: 60/056,884
/ EARLIER FILING DATE: 1997-08-22
/ EARLIER APPLICATION NUMBER: 60/057,669
/ EARLIER FILING DATE: 1997-09-05
/ EARLIER APPLICATION NUMBER: 60/049,610
/ EARLIER FILING DATE: 1997-06-13
/ EARLIER APPLICATION NUMBER: 60/061,060
/ EARLIER FILING DATE: 1997-10-02

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Query Match 26.9%; Score 179.2; DB 3; Length 1285;
Best Local Similarity 58.5%; Pred. No. 2,6e-54;
Matches 332; Conservative 0; Mismatches 233; Indels 3; Gaps 1;

Qy 47 TTGGATTACGGCTTTCTTTCGAGCATGAGGCTGTGCGAAGAGGCAAAATCCGTT 106
Db 145 TGGTTTACGAGCTGTGCTTACAGTTTATTAAGAAACTGTAACTGCTATT 204
Qy 107 TCTGGTCTCGACATGCTGCGACAGTACTCTTTCGACATGCTCAAGATGAAACT 166
Db 205 TCTTGGATTGATATGACGAGAAACAAATGCTACATGCTAATAAATGACAGACT 264
Qy 167 GGGGCAACATCAACCAACGAGTATCCAGCTCAGAGGAGTTGATATCAACAGATGAA 226
Db 265 TGGCAACATGTCCCAACATTCACCTCCAGAACTGACCATTCCTGCGACACT 324
Qy 227 GTTCAAGCATGATGCTGGGTGCGCACACATGCTCGAAGGCTGGAAGGAGCTACTA 286
Db 325 GTTTACAACTTTTGTATGCTGGGTGACATGTTCAAGCTCGAAGAGTGGAAAACTA 384
Qy 287 TGCTAAGGTGATGCTATGATGATCTGCTGACGCGAGTACAGGAGGAGATTTGCTGA 346
Db 385 TCGTGTATCAATGAGCATTTGATTTCTGTGGATTTGACAGCAAGAAAGGCTTTAGA 444

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Qy 347 GTCAAGAAAGAGCTGATTTCTTCTCTCCAGCATTTCTGTCCAGTTCTGTGCT 406
Db 445 GTCAAGAAAGAGCTGATTTCTTCTCTCCAGCATTTCTGTCCAGTTCTGTGCT 504
Qy 407 CCTCTGGGAAACAAATGATATCCCGTCTTCTTGAAGAGAGTTGCGTTGAC 466
Db 505 GATTTCTGGGAAATTAAGATGACGACCTGACCATTCAGTGAAGAGAGTTGCG 564
Qy 467 ACTGGGTGACCAT---GACCACTGTAAAGAAAGGTAACCTGGAGATAGCAACT 523
Db 565 GTTTGTTATATGCTGACACAAAGAAAGGAGTATATCTTGAAGAACTGAAATC 624
Qy 524 TCGGCCATTGAGTTTTCATGTCAGATATGTCGCAAAATGGGGTACGTTGAA 583
Db 625 CCGACCTTGAAGAGTTTTCATGTTAGTGTCTCAAAAGCAAGGTTGAGGAAGCTT 684
Qy 584 CAATGATGATCCAGTACATCAAGTGA 611
Db 685 CCGCTGATGACAGTACATGATTTAA 712

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RESULT 8
US-09-533-559-125
/ Sequence 125, Application US/09533559
/ Patent No. 6902887
/ GENERAL INFORMATION:
/ APPLICANT: Randy M. Berka
/ APPLICANT: Michael W. Rey
/ APPLICANT: Jeffrey R. Shuster
/ APPLICANT: Sakari Kauppinen
/ APPLICANT: Ib Groth Clausen
/ APPLICANT: Peter Bjarke Olsen
/ TITLE OF INVENTION: Methods For Monitoring Multiple Gene
/ FILE REFERENCE: 5849.200-US
/ CURRENT APPLICATION NUMBER: US/09/533,559
/ CURRENT FILING DATE: 2000-03-22
/ EARLIER APPLICATION NUMBER: 09/273,623
/ EARLIER FILING DATE: 1999-03-22
/ NUMBER OF SEQ ID NOS: 7860
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 125
/ LENGTH: 1700
/ TYPE: DNA
/ ORGANISM: Fusarium venenatum
/ FEATURE:
/ NAME/KEY: misc.feature
/ LOCATION: (1)...(1700)
/ OTHER INFORMATION: n = A,T,C or G
US-09-533-559-125

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Query Match 26.2%; Score 174.8; DB 3; Length 1700;
Best Local Similarity 60.7%; Pred. No. 1.3e-52;
Matches 320; Conservative 0; Mismatches 200; Indels 7; Gaps 2;

Qy 30 ACCATTTCTTCTGATTTGATTTTACGCTTTCTTTCGACATAGGCTGTGCGAAG 89
Db 109 ATCATGTGATGTCACACGTTTCTAAGATGTGTCTCTCTGGGCTGTGCAACAG 168
Qy 90 GAGGCCAAATCTGTTTCTGAGTCTGACAAATGCTGCAAGACTCTTCTGACATG 149
Db 169 CAGCAAGCTGTTTCTCTGCTTTCGACAAAGCGGAAAGACTTCTTCTCCACATG 228
Qy 150 CTCGAAGATGAGAACTGGGGGCAATCAACGACGATATTCACGTCAGAGAGTTG 209
Db 229 CTGAAGACGACGATGTCATTCACAGCCACTTCAACCCGACATCCAGAGAGTT 288
Qy 210 AGTATCAACAGATGATGTTCAAGATTTGATGCTGGGTGCGACACATGCTGAG 269
Db 289 GCTATTGTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 348
Qy 270 GTGTGAGGAGACTATATCTAAGGTGATGATATGATATCTGTCAGCAGATGAG 329

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Db 349 ATCTGGGCGATTAATCTCCCGAGGTCAACGGTGTCTTCTTATGACGCGCAAGAC 408
Qy 330 AGGAGGATTTGTGATGCAAAAGAAAGCTCGATTTCTTCTCCGACGATTTCTG 389
Db 409 CACAGCGATTTGTGATGCAAAAGAAAGCTCGATTTCTTCTCCGACGATTTCTG 468
Qy 390 TCCCAATTTCTGTGCTGTCTGTGGAACAAAGATTAATCCGTAAGCTTTCTGAA 449
Db 469 TCCAAAGTTCTTGTATCTCTCGGCAACAAAGATCAACACCCG-ATGCGTCTCCGAA 527
Qy 450 GACAGTTGGGCTTCACTTGGGTTGACCATGACCTGTGAAGAAAGGTAACCTG 509
Db 528 GACCAAAATGCAACCAACTGGCTCTTACCAAAACCGGTAAAGGCAAGGTCACCTT 587
Qy 510 GGAGATAGCAACATTCGCGCCATGAGGTTTTCATGTGCAATTTGT 556
Db 588 GAGG-----GCATCCGACCTATTGAGCTCTTCAATGTCTCANTAGT 628

RESULT 9

US-09-016-434-913
Sequence 913, Application US/09016434
Patent No. 6500938

GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 913:
SEQUENCE CHARACTERISTICS:
LENGTH: 903 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: TONSNOT01
CLONE: 735249
US-09-016-434-913

Query Match 25.5%; Score 169.8; DB 3; Length 903;
Best Local Similarity 58.4%; Pred. No. 5,66-51;
Matches 316; Conservative 0; Mismatches 222; Indels 3; Gaps 1;
Qy 46 ATTGGTTTACGGCTTTCTTGGCAGCATAGGGCTGTGGCAGAAAGAGGCCAAAATCTCTGT 105

Db 237 ATGGCTTACAGAGTGTGCTCCAGTTCTCTAGGACTGTACAGAAATCTGAAAACTTGAT 296
Qy 106 TTCTGGGCTTCGCAATAGCTGCGAAGACTATCTTTGTGACATGCTCAAGATGAGAAAC 165
Db 297 TCTTAGGTTTGAATATGACAGGCAAAACACTTTCTTCAATGCTCAAAAGATGACAGAT 356
Qy 166 TGGGGCAATCAACCAACGCAAGTATCCACGTCAGAGAGTTAGTATCAACAGATGA 225
Db 357 TGGGCCAATATGTTCAACACTATCCATCCATCAAGAAAGCTAACAAATGTGCTGAATGA 416
Qy 226 AGTTCAAAACATTCGATCTGGGTGCGACACATATGCTGTGAGCGGTGGAAGGAACTACT 285
Db 417 CTTTACAACTTTGATCTTGTGGGCAAGACAGCAACAGCTGCGTTTGAATAATATC 476
Qy 286 ATGCTAAGGTGATGCTATATGATATCTGTGACCGCAGTACAGAGAGATTTGCTG 345
Db 477 TCCACACATTAATGGATTTGCTTCTGTGTGACCTGTGCAAGTATCTCGCTGTGG 536
Qy 346 AGTCAAAAGAAAGCTCGATTTCTTCTCCGACATTTCTGTCCAAAGTTCTGTGC 405
Db 537 AATCCAAAGTTGAGCTTAATGCTTATGACTGATGAAACAAATATCCAAATGTGCCAATCC 596
Qy 406 TCGTCTGGGAAACAAAGATTAATCCCGTACGCTTCTGAAAGCAGATTGCGGTTCA 465
Db 597 TTATCTTGGGTAAACAAATTTGACAGAACAGATGCAATGAGTGAAGAAAACTCCGTGAGA 656
Qy 466 CACTTGGGTTGACCAT---GACCACTGTGTAAGAAACGCTGAACCTGGAGATGACACA 522
Db 657 TATTGGGCTTTATGACACAGACACAGAAAGGGAATGTGACCTGGAAGAGCTGAATG 716
Qy 523 TTGGGCCCATTTAGGTTTTCATGTGCAAGTATGTGCGCAAAATGGGCTACGTTAAGTT 582
Db 717 CTCGCCCATGGAAGTTGATGTGCAAGTGTGCTCAAGAGGCCAAGGTTACGGCGAAGGGGT 776
Qy 583 T 583
Db 777 T 777

RESULT 10

US-09-248-796A-6222
Sequence 6222, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstein et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248, 796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074, 725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096, 409
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 6222
LENGTH: 564
TYPE: DNA
ORGANISM: Candida albicans
US-09-248-796A-6222

Query Match 24.6%; Score 164; DB 3; Length 564;
Best Local Similarity 58.1%; Pred. No. 5,4e-49;
Matches 309; Conservative 0; Mismatches 220; Indels 3; Gaps 1;
Qy 73 TAGGGCTGTGCGAAGAGGCGCAAAATCTGTTCTGAGTCTCGCAATGCTGCGAAGA 132
Db 32 TAGGATTAATGAAATTAACATGCAAAATTAATTTTAAAGGTTAAGATTAATGCTGTAATA 91

Qy 133 CTACTCTTTCGCAATGCTCAAGATGAGAAAATGGGGCAACATCAACCAAGCAATATC 192
Db 92 CTACTCTTTTACATATGTTAAAGAAATGATGATGGCCACTTTTACCAACCAATTAATATC 151

SEQ ID NO 445
LENGTH: 504
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 141..503
US-09-621-976-445

Query Match 17.3%; Score 115.2; DB 3; Length 504;
Best Local Similarity 58.9%; Pred. No. 3.5e-31;
Matches 198; Conservative 0; Mismatches 138; Indels 0; Gaps 0;

QY 46 ATTGGTTTACGGCTTCTTCGAGCATAGGCGCTGTGGCAAGAGCCAAATCTGT 105
DB 169 ATGGCTTCACAGTGTGCTCCAGTCTCTAGAGACTGTACAGAAATCTGAAAACTGTAT 228
QY 106 TTTCGGGTTCGACATGCTGGCAGACTACTCTTTCGACATGCTCAAGATGAGAAC 165
DB 229 TCTTAGGTTTGATTAAGCAGGCAAAACACTCTTTCACATGCTCAAGATGACAGAT 288
QY 166 TGGGGCAACATCAACCAAGCAGATCAACGTCAGAGAGTTGATCAACAGAGTGA 225
DB 289 TGGGCCACATGTTCTTCAACACTACATCCAGATCAGAAAGCTAACATTTGCTGGAATGA 348
QY 226 AGTTCAAGCATTCGATCTGGTGGCCACACAAATGCTCGACGCGTGTGAGGAGCTACT 285
DB 349 CTTTACACATTTTGAATCTTGTGGGACGAGCAAGRCGTGGGTTTGGAAAAATATATC 408
QY 286 ATGCTAAGGTGATGCTATGATGATCTCTGACGCAAGTACAGAGGAGATTTCTG 345
DB 409 TCCGAGCAATTAAGGATGTTCTTCTGTGGAGCTGTGAGATCATTTCTGCTCGTGG 468
QY 346 AGTCAAGAAAGAGCTGATCTCTCTCTCCGAG 381
DB 469 ATCCAAAGTTGAGCTTAATGCTTAATGACTGATG 504

RESULT 14

US-09-016-434-501
Sequence 501, Application US/09016414
Patent No. 650038

GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Sellhammer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 501:
SEQUENCE CHARACTERISTICS:
LENGTH: 262 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PROSONO1
CLONE: 2278736
US-09-016-434-501

Query Match 14.3%; Score 95.4; DB 3; Length 262;
Best Local Similarity 62.2%; Pred. No. 3.8e-24;
Matches 150; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

QY 73 TAGGGCTGTGGCAAGAGAGCCAAATCTGTTTCTGGGTCTCGACATAGCTGGCAAGA 132
DB 21 TAGGATTAATTAAGAAACTGTAACTGTATTTCTTGATTTGATTAAGAGAAAAA 80
QY 133 CTACTCTTTCGACATGCTCAAGATGAGAACTGGGGCAACATCAACAGCAGATATC 192
DB 81 CAACATTTCTACATGCTTAAGATGACAGACTTGGACAAACATGCCAACATTAATC 140
QY 193 CAACGTGAGAGAGTTGATGATCAACAGAGTGAAGTTCAAGCATTGATCTGGGTGGCC 252
DB 141 CGACTTCGAGAAATGACCATATGCTGGCATGACGTTTACACTTTTGAATCTGGGTGAC 200
QY 253 ACACAATGCTGACGCTGTGAGAGGACCTACTATGCTAAGGTGATGCTATGCTATC 312
DB 201 ATGTTCAAGCTCGAAGAGTGTGAAAAAATACCTTCTGCTATCAATGAGATGATTTTC 260
QY 313 T 313
DB 261 T 261

RESULT 15

US-09-513-999C-10983
Sequence 10983, Application US/09513999C
Patent No. 6783961

GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
PATENT NO. 6783961
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 10983
LENGTH: 587
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 426-
OTHER INFORMATION: m=a or c
US-09-513-999C-10983

Query Match 13.8%; Score 92.2; DB 3; Length 587;
Best Local Similarity 65.1%; Pred. No. 9.8e-23;
Matches 136; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 46 ATTGGTTTACGGCTTCTTCGAGCATAGGCGCTGTGGCAAGAGCCAAATCTGT 105
DB 156 ATGGCTTCACAGTGTGCTCCAGTCTCTAGAGACTGTACAGAAATCTGAAAACTGTAT 215

Qy	106	TTCTGGGCTCGACATGCTGGCAAGACTCTTCTGACATGCTCAAGATGAGAAAC	165
Db	216	TCTTAGGTTTGATTAATGAGGCAAAACACTCTTCTCAATGCTCAAGATGACAGAT	275
Qy	166	TGGGGCAACATCAACCAACGCAAGTATCCAACTGAGAGAGTTGAGTATCAACAGATGA	225
Db	276	TGGGCCAACATGTTCCAACTACATCCGACATCAGAGAGCTTAACAATTGCTGGAATGA	335
Qy	226	AGTTCAAAGCATTCGATCTGGGTGGCCAC	254
Db	336	CCTTTACAACCTTTGATCTTGGTGGGCAC	364

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OM nucleic - nucleic search, using sw model

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Title: US-10-688-481-6

Perfect score: 667

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Searched: 9793542 seqs, 4134689005 residues

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications NA Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	667	100.0	667	3 US-09-828-310-6	Sequence 6, Appl 1
2	667	100.0	667	8 US-10-688-481-6	Sequence 6, Appl 1
3	655	98.2	805	3 US-09-828-310-1	Sequence 1, Appl 1
4	655	98.2	805	8 US-10-688-481-1	Sequence 1, Appl 1
5	349.6	52.4	954	7 US-10-767-701-13805	Sequence 13805, A
6	340.4	51.0	954	7 US-10-425-114-7242	Sequence 7242, Ap
7	340.4	51.0	1221	8 US-10-425-115-143342	Sequence 143342, A
8	340.4	51.0	1645	8 US-10-425-115-143343	Sequence 143343, A
9	338.4	50.7	1070	8 US-10-425-115-98353	Sequence 98353, A
10	335.6	50.3	955	7 US-10-425-114-21639	Sequence 21639, A
11	332.4	49.8	966	7 US-10-425-114-13536	Sequence 13536, A
12	332.4	49.8	1017	7 US-10-425-114-33380	Sequence 33380, A
13	332.4	49.8	1334	8 US-10-425-115-98354	Sequence 98354, A
14	330.4	49.5	966	7 US-10-425-114-20345	Sequence 20345, A
15	330.4	49.5	1051	7 US-10-425-114-20291	Sequence 20291, A
16	330.4	49.5	1073	7 US-10-425-114-378	Sequence 378, App
17	330.4	49.5	1117	7 US-10-425-114-27102	Sequence 27102, A
18	330.4	49.5	1137	8 US-10-425-115-143340	Sequence 143340, A
19	329.2	49.4	1164	7 US-10-425-114-26805	Sequence 26805, A
20	328.8	49.3	928	7 US-10-767-701-15389	Sequence 15389, A
21	326.2	48.9	1688	7 US-10-437-963-58339	Sequence 58339, A
22	326	48.9	1184	7 US-10-437-963-45082	Sequence 45082, A
23	324	48.6	1036	7 US-10-424-599-31196	Sequence 31196, A

24	321.4	48.2	991	7 US-10-424-599-13515	Sequence 13515, A
25	320	48.0	1303	8 US-10-425-115-143338	Sequence 143338, A
26	319.6	47.9	1191	7 US-10-424-599-139806	Sequence 139806, A
27	318.8	47.8	928	7 US-10-425-114-11886	Sequence 11886, A
28	318.8	47.8	1132	7 US-10-424-599-13513	Sequence 13513, A
29	313	46.9	807	8 US-10-767-795-1302	Sequence 1302, Ap
30	312.8	46.9	994	8 US-10-767-795-1303	Sequence 1303, Ap
31	312.6	46.9	1047	8 US-10-767-795-1304	Sequence 1304, Ap
32	296.6	44.5	592	7 US-10-021-323-15172	Sequence 15172, A
33	295	44.2	675	3 US-09-770-149-379	Sequence 379, App
34	292.2	43.8	811	8 US-10-425-115-140995	Sequence 140995, A
35	288.8	43.3	1164	7 US-10-424-599-32367	Sequence 32367, A
36	283.8	42.5	764	7 US-10-424-599-32368	Sequence 32368, A
37	275	41.2	1066	7 US-10-424-599-142530	Sequence 142530, A
38	272.6	40.9	569	7 US-10-021-323-15674	Sequence 15674, Ap
39	262.8	39.4	603	7 US-10-021-323-11457	Sequence 11457, A
40	262	39.3	570	8 US-10-425-115-12354	Sequence 12354, A
41	220.6	33.1	692	7 US-10-437-963-55941	Sequence 55941, A
42	218.8	32.8	570	5 US-10-128-714-2426	Sequence 2426, Ap
43	216	32.4	992	10 US-11-097-143-15608	Sequence 15608, A
44	215.6	32.3	570	5 US-10-128-714-7426	Sequence 7426, Ap
45	213	31.9	660	7 US-10-437-963-20654	Sequence 20654, A

ALIGNMENTS

RESULT 1

US-09-828-310-6

Sequence 6, Application US/0928310

Patent No. US20020066124A1

GENERAL INFORMATION:

APPLICANT: COSTA E SILVA, OSWALDO DA

APPLICANT: BOHNETT, HANS J.

APPLICANT: VAN THIELEN, NOCHA

APPLICANT: CHEN, ROUYING

TITLE OF INVENTION: GTP BINDING STRESS-RELATED PROTEINS AND METHODS OF USE

TITLE OF INVENTION: IN PLANTS

FILE REFERENCE: 16313-0039

CURRENT APPLICATION NUMBER: US/09/828,310

CURRENT FILING DATE: 2001-04-06

PRIOR APPLICATION NUMBER: 60/196,001

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 50

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 6

LENGTH: 667

TYPE: DNA

ORGANISM: Physcomitrella patens

US-09-828-310-6

Query Match 100.0%; Score 667; DB 3; Length 667;

Best Local Similarity 100.0%; Pred. No. 2.5e-220;

Matches 667; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCCCGGTCCTGATGATACCAAGGCTGTAACATGTTCTTGATGATGTTTACGGCT 60

DB 1 ATCCCGGTCCTGATGATACCAAGGCTGTAACATGTTCTTGATGATGTTTACGGCT 60

QY 61 TTCTTGCGAGCATATGAGGCTGTGCGAGAGAGGCAAAATCTGTTCTGAGTCTGACA 120

DB 61 TTCTTGCGAGCATATGAGGCTGTGCGAGAGAGGCAAAATCTGTTCTGAGTCTGACA 120

QY 121 ATGCTGCAAGACTACTTCTTGACATGCTCAAGATGAGAAATCGGGCAATCAAC 180

DB 121 ATGCTGCAAGACTACTTCTTGACATGCTCAAGATGAGAAATCGGGCAATCAAC 180

QY 181 CAACGAGATATCAAGTCAAGAGATGATGATCAACGAGATGATCAAGATGATGATG 240

DB 181 CAACGAGATATCAAGTCAAGAGATGATGATCAACGAGATGATGATGATGATG 240

QY 241 ATCTGGTGGCCACATGCTGCAAGGCTGAGAGGAGTCACTACTGATGATGATGATG 300

Db 241 ATCTGGGTGACACACATGCTTCGACGCGTGTGGAGGACCTACTATGTAAGTGGATG 300
Qy 301 CTATAGTATCTCTGTCGACGACGATAGACAGGAGAGATTTGCTGAGTCAAGAAAGAGC 360
Db 301 CTATAGTATCTCTGTCGACGACGATAGACAGGAGAGATTTGCTGAGTCAAGAAAGAGC 360
Qy 361 TCGATTCTCTCTCTCGGAGATTTCTCTGTCGACGATTTCTGCTGCTGCTGCTGAGAAAC 420
Db 361 TCGATTCTCTCTCTCGGAGATTTCTCTGTCGACGATTTCTGCTGCTGCTGCTGAGAAAC 420
Qy 421 AGATTGATATCCCGTACGCTTTCTTGAAGACGATTTGCGGTTTCACTTGGGTTGACCA 480
Db 421 AGATTGATATCCCGTACGCTTTCTTGAAGACGATTTGCGGTTTCACTTGGGTTGACCA 480
Qy 481 TGACCACTGGTAAAGAAAGGATGAACTTGGAGATAGCAATTCGCGCCATTGAGGTTT 540
Db 481 TGACCACTGGTAAAGAAAGGATGAACTTGGAGATAGCAATTCGCGCCATTGAGGTTT 540
Qy 541 TCATGTCAGATATTGTGCGCAAAATGGGGTACGGTGAAGGTTTCAAGTGAATGACCAAGT 600
Db 541 TCATGTCAGATATTGTGCGCAAAATGGGGTACGGTGAAGGTTTCAAGTGAATGACCAAGT 600
Qy 601 ACATCAAGTATTTGTTTCTCTGTAAGAGAACTTAGCTCGGTTTAAAGAGGACGAG 660
Db 601 ACATCAAGTATTTGTTTCTCTGTAAGAGAACTTAGCTCGGTTTAAAGAGGACGAG 660
Qy 661 TTAACGC 667
Db 661 TTAACGC 667

RESULT 2

US-10-688-481-6
; Sequence 6, Application US/10688481
; Publication No. US20040194163A1
; GENERAL INFORMATION:
; APPLICANT: COSTA E SILVA, OSMALDO DA
; APPLICANT: BOHNER, HANS J.
; APPLICANT: VAN THIELEN, NOCHA
; APPLICANT: CHEN, ROUYING
; TITLE OF INVENTION: GTP BINDING STRESS-RELATED PROTEINS AND METHODS OF USE
; TITLE OF INVENTION: IN PLANTS
; FILE REFERENCE: 16313-0039
; CURRENT APPLICATION NUMBER: US/10/688,481
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/196,001
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO: 6
; LENGTH: 667
; TYPE: DNA
; ORGANISM: Physcomitrella patens
US-10-688-481-6

Query Match 100.0%; Score 667; DB 8; Length 667;
Best Local Similarity 100.0%; Pred. No. 2,5e-220;
Matches 667; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATCCCGGTCCTGATACCAAGCTGTACCATGTTTCTGTGATTTGTTTACGGCT 60
Db 1 ATCCCGGTCCTGATACCAAGCTGTACCATGTTTCTGTGATTTGTTTACGGCT 60
Qy 61 TTCTTGGAGCATGAGGCTGTGGCAGAAAGAGGCAAAATCTGTTTCTGGGCTCGACA 120
Db 61 TTCTTGGAGCATGAGGCTGTGGCAGAAAGAGGCAAAATCTGTTTCTGGGCTCGACA 120
Qy 121 ATGCTGGCAAGACTACTTCTTGCACATGCTCAAGATGAGAACTGGGCGCAATCAAC 180
Db 121 ATGCTGGCAAGACTACTTCTTGCACATGCTCAAGATGAGAACTGGGCGCAATCAAC 180
Qy 181 CAAGCAGTATCAAGCTCAGAGAGTTGAGTATCAACAGATGAGTCAAGACATTGG 240
Db 181 CAAGCAGTATCAAGCTCAGAGAGTTGAGTATCAACAGATGAGTCAAGACATTGG 240

Db 181 CAAGCAGTATCAAGCTCAGAGAGTTGAGTATCAACAGATGAGTCAAGACATTGG 240
Qy 241 ATCTGGGTGACACACATGCTTCGACGCGTGTGGAGGACCTACTATGTAAGTGGATG 300
Db 241 ATCTGGGTGACACACATGCTTCGACGCGTGTGGAGGACCTACTATGTAAGTGGATG 300
Qy 301 CTATAGTATCTCTGTCGACGACGATAGACAGGAGAGATTTGCTGAGTCAAGAAAGAGC 360
Db 301 CTATAGTATCTCTGTCGACGACGATAGACAGGAGAGATTTGCTGAGTCAAGAAAGAGC 360
Qy 361 TCGATTCTCTCTCTCGGAGATTTCTCTGTCGACGATTTCTGCTGCTGCTGCTGAGAAAC 420
Db 361 TCGATTCTCTCTCTCGGAGATTTCTCTGTCGACGATTTCTGCTGCTGCTGCTGAGAAAC 420
Qy 421 AGATTGATATCCCGTACGCTTTCTTGAAGACGATTTGCGGTTTCACTTGGGTTGACCA 480
Db 421 AGATTGATATCCCGTACGCTTTCTTGAAGACGATTTGCGGTTTCACTTGGGTTGACCA 480
Qy 481 TGACCACTGGTAAAGAAAGGATGAACTTGGAGATAGCAATTCGCGCCATTGAGGTTT 540
Db 481 TGACCACTGGTAAAGAAAGGATGAACTTGGAGATAGCAATTCGCGCCATTGAGGTTT 540
Qy 541 TCATGTCAGATATTGTGCGCAAAATGGGGTACGGTGAAGGTTTCAAGTGAATGACCAAGT 600
Db 541 TCATGTCAGATATTGTGCGCAAAATGGGGTACGGTGAAGGTTTCAAGTGAATGACCAAGT 600
Qy 601 ACATCAAGTATTTGTTTCTCTGTAAGAGAACTTAGCTCGGTTTAAAGAGGACGAG 660
Db 601 ACATCAAGTATTTGTTTCTCTGTAAGAGAACTTAGCTCGGTTTAAAGAGGACGAG 660
Qy 661 TTAACGC 667
Db 661 TTAACGC 667

RESULT 3

US-09-828-310-1/c
; Sequence 1, Application US/09828310
; Patent No. US20020066124A1
; GENERAL INFORMATION:
; APPLICANT: COSTA E SILVA, OSMALDO DA
; APPLICANT: BOHNER, HANS J.
; APPLICANT: VAN THIELEN, NOCHA
; APPLICANT: CHEN, ROUYING
; TITLE OF INVENTION: GTP BINDING STRESS-RELATED PROTEINS AND METHODS OF USE
; TITLE OF INVENTION: IN PLANTS
; FILE REFERENCE: 16313-0039
; CURRENT APPLICATION NUMBER: US/09/828,310
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/196,001
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO: 1
; LENGTH: 805
; TYPE: DNA
; ORGANISM: Physcomitrella patens
US-09-828-310-1

Query Match 98.2%; Score 655; DB 3; Length 805;
Best Local Similarity 100.0%; Pred. No. 4.1e-216;
Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CGGGTCGTGATACCAAGGCTGTACCATGTTTCTGTGATTTGTTTACGGCTTTCT 64
Db 781 CGGGTCGTGATACCAAGGCTGTACCATGTTTCTGTGATTTGTTTACGGCTTTCT 722
Qy 65 TGGAGCATAGGCTGTGGCAGAAAGAGGCAAAATCTGTTTCTGGGCTCGACAATGC 124
Db 721 TGGAGCATAGGCTGTGGCAGAAAGAGGCAAAATCTGTTTCTGGGCTCGACAATGC 662
Qy 125 TGGCAAGTACTCTTCTTGCACATGCTCAAGATGAGAACTGGGCGCAATCAAC 184
Db 125 TGGCAAGTACTCTTCTTGCACATGCTCAAGATGAGAACTGGGCGCAATCAAC 184

[illegible]

Db	66	TGGCAAGA	CTA	CTTTGCA	CACTGCTCA	AGATGAGAAA	CTGGGCA	AATCA	CAAC	602
Qy	185	GCAGTAT	CCA	AGTCAG	AGATTG	AGATCA	CAAGTGA	AGTTCA	AGATTCG	244
Db	601	GCAGTAT	CCA	AGTCAG	AGATTG	AGATCA	CAAGTGA	AGTTCA	AGATTCG	542
Qy	245	GGGTGG	CCA	CAATTC	GTCTGA	CGCGTGTG	AGGGGACT	ACTATG	CTAAGTGTG	304
Db	541	GGGTGG	CCA	CAATTC	GTCTGA	CGCGTGTG	AGGGGACT	ACTATG	CTAAGTGTG	482
Qy	305	AGTGTAT	CTC	GTGCA	CGCAGT	AGACAGG	GAAGATTT	GTGATCA	AGAAAGATCT	364
Db	481	AGTGTAT	CTC	GTGCA	CGCAGT	AGACAGG	GAAGATTT	GTGATCA	AGAAAGATCT	422
Qy	365	TTCTCTT	CTC	CCGAC	GAATTC	CTCTGCC	AAATTC	CTGTGCT	CTGCGGAAA	424
Db	421	TTCTCTT	CTC	CCGAC	GAATTC	CTCTGCC	AAATTC	CTGTGCT	CTGCGGAAA	363
Qy	425	TGATAT	CCCGTA	CGCTTCT	GTGA	AGACGAGT	GGGTTCA	CACTTG	GGGTTGAC	484
Db	361	TGATAT	CCCGTA	CGCTTCT	GTGA	AGACGAGT	GGGTTCA	CACTTG	GGGTTGAC	302
Qy	485	CACTGT	TAA	AGGAAC	GGGGAAC	CTGGAGAT	AGCAAC	ATTGGG	CCATTGAGGTTT	544
Db	301	CACTGT	TAA	AGGAAC	GGGGAAC	CTGGAGAT	AGCAAC	ATTGGG	CCATTGAGGTTT	242
Qy	545	GTGCA	GATAT	TGTG	CGCAAAAT	TGGGGTAC	GGTGA	AGGTTCA	AGTGA	604
Db	241	GTGCA	GATAT	TGTG	CGCAAAAT	TGGGGTAC	GGTGA	AGGTTCA	AGTGA	182
Qy	605	CAAGTAT	TGTTT	CTGTG	AAAGGAA	CACTTA	GCTGGT	GTATTAA	GGGAGGA	659
Db	181	CAAGTAT	TGTTT	CTGTG	AAAGGAA	CACTTA	GCTGGT	GTATTAA	GGGAGGA	127

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RESULT 4
US-10-688-481-1/C
; Sequence 1, Application US/10688481
; Publication No. US20040194163A1
; GENERAL INFORMATION:
; APPLICANT: COSTA E SILVA, OSMILDO DA
; APPLICANT: BOHNERT, HANS J.
; APPLICANT: VAN THIELEN, NOOCHA
; TITLE OF INVENTION: GTP BINDING STRESS-RELATED PROTEINS AND METHODS OF USE
; TITLE OF INVENTION: IN PLANTS
; FILE REFERENCE: 16313-0039
; CURRENT APPLICATION NUMBER: US/10/688,481
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/196,001
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 805
; TYPE: DNA
; ORGANISM: Physcomitrella patens
US-10-688-481-1

          98.2%; Score 655; DB 8; Length 805;
Query Match Best Local Similarity 100.0%; Pred. No. 4,1e-216; Indels 0; Gaps 0
Matches 655; Conservative 0; Mismatches 0;

QY      5  CGGGTCGTGATACCAAGGCTGTGATCAATGTTCTTGATGATGAGTTTACGGCTTCT 64
Db      781 CGGGTCGTGATACCAAGGCTGTGATCAATGTTCTTGATGATGAGTTTACGGCTTCT 722
QY      65  TGCAGCATATGGGCTGTGGCAGAAGAGGCAAAATCTCTGTTCTGGGCTTCGACATGC 125
Db      721 TGCAGCATATGGGCTGTGGCAGAAGAGGCAAAATCTCTGTTCTGGGCTTCGACATGC 667
QY      125 TGCAGCATATCTTCTGCAATGCTCAAGATGAGAACTGGGGGCAATCAACCAAC 187

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RESULT 5
US-10-767-701-13805
; Sequence 13805, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5353)B
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 13805
; LENGTH: 954
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAV03-CLUS2820_1
US-10-767-701-13805

Query Match          52.4%; Score 349.6; DB 7; Length 954;
Best Local Similarity 76.4%; Pred. No. 5.7e-110;
Matches 443; Conservative 0; Mismatches 134; Indels 3; Gaps 1;

QY      ATGTTTCTTGAGATGGTTTTTAACGGCTTCTTGGCAGATAGGGCGTCGGAGAAGAG 92
DB      |||||
DB      134 ATGTTCCTGGAGACTGTGTTCTACCGGGGTGCTGGCGCTTGCGCTGTGGCAAGAG 193
QY      GCCAAATCCTGTTTCTGGGTCCTGCACATGCTGGCAAGACTACTCTTCTGCACATGCTC 152
DB      |||||
DB      194 GCAGAGATCTCTTCTCTCGGCTGCACAACGCCGCAAGACCACCTCTCCACATGCTC 253
QY      AAGGATGAAGAACTGGGGCAAATCAACCAAAGCAGTATCCAAAGTCAGAGGAGTTGAGT 212
DB      |||||
DB      254 AAGGACGAGCGGCTGTGTCCAGCACCAAGCGACAGTAGTACCGACGTCAGAAAGAGCTGAGC 313

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QY 213 ATCAACAGAGTGAAGTTCAAAAGCATTCGATCTGGGTGGCCACACATCGCTCGACGGT 272
DB 314 ATGGCGAGGATCAAGTTCAAGGCGCTTGACCTCGGGGGCCACAGATCGCTCGCGGGT 373
QY 273 TGGAGGACTACTATGCTAAGGTGATGCTATAGTGTATCTCGTCAAGCAGTAGACAG 332
DB 374 TGGAGGATTAACACGAAAGGTTGATGCTGTAGTATACCTGGTAGTACATAGACAG 433
QY 333 GAGAGATTTGCTGAGTCAAAAGAAAGAGCTCGATTTCTTCTCTCGACAGATTTCTGTCC 392
DB 434 GAGGATTTGCAAAATCAAAAAGAGCTCGATGCTCTCGTGTGATGATTCCTTGGCC 493
QY 393 CAAGTCTGTGCTGCTGCTGGGAAACAAATGATATCCCGTATGCTTCTTGAAGAC 452
DB 494 AATGTTCCATTTTCGATCTTGGCAACAAATGATATCCCATATGCTGCTCTGAAGAG 553
QY 453 GAGTGGCGTTCACTTGGGTTGACCA--TGACCACTGGTAAAGAAAGGTAACCTG 509
DB 554 GAGCTACGGTATCACTTACGCTTACGCACTTCAACACGGGAAGGCAAGTCACTT 613
QY 510 GGAAGTACCAATTCGCGCCATTGAGGTTTCAATGTCAGATATGTCGCAAAATGGGG 569
DB 614 GGTGATCCCAATGTCGGGCCACTTGAAGTTTTCATGTGCAAGTGTGTTCCCAAGATGGC 673
QY 570 TACGTTGAAGTTTCAAGTGTGATGACCCAGTACATCAAGT 609
DB 674 TACGTTGATGTTTCAAGTGTGCTCCAGTACATCAAGT 713
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RESULT 6

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US-10-425-114-7242
; Sequence 7242, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaka, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 7242
; LENGTH: 998
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700623579_F11
US-10-425-114-7242
```

Query Match 51.0%; Score 340.4; DB 7; Length 998;
Best Local Similarity 74.7%; Pred. No. 9.1e-107;
Matches 441; Conservative 0; Mismatches 146; Indels 3; Gaps 1;

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QY 23 GGCTGTACCAATGTTCTTGTAGATGTTTACGGCTTCTTGCAGCATAGGGCTGTG 82
DB 156 GGTGGGGAAGATGTTCTCTGGGACTGGTCTACGGGGTGTGGCTCCCTCGGCTGTG 215
QY 83 GCAGAGGAGGCAAAATCTGTTTCTGGGTCTGCAGATGCTGGCAAGACTACTTCT 142
DB 216 GCAGAGGAGGCAAAATCTCTTCTTGGCTCGACAAAGCGGCAAGACAGCTGCT 275
QY 143 GCACATGCTCAAGATGAGAACTGGGGCAACATCAACGACGATTCACAGTCA 202
DB 276 CCACATGCTCAAGACGAGCGGTTGTGACACACGACGACGACGACGACGACG 335
QY 203 GGAATTAAGTATCAACAGATGAGATTCGAAGCATTCGATCGGTGGCCACAAATCG 262
DB 336 GGAAGTCAAGATCGCAAGATCAAGTCAAGCGTTGACCTCGGCGCCACAGATCG 395
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QY 263 TCGACCGCTGTGGAGGACCTATGCTAAGGTGATGCTATAGTATCTCGTCAAGC 322
DB 396 GCGCCCGCTGTGGAGGATTAACACCAAGGTTGATGCTGATGATTAACCTGGTAGATG 455
QY 323 AGTAGACAGGAGAGATTTGCTGAGTCAAAAGAAAGCTGATTTCTTCTCTCCGACGA 382
DB 456 ATATGATTAAGAGACGATTTGCTGATCAAAAGAGAGCTGATGCTCTCTGCTATGA 515
QY 383 TTCTGTGCTCAAGTCTGTGTCTGCTCGGAAACAAATGATATCCGTACCTTC 442
DB 516 TTCTTTGGCAATGTTCCATTTCTCATCTTGGCAACAGATGATATCCATATGCTGC 575
QY 443 TTCTGAAGACAGATTCGGTTACACTTGGGTTGACCA--TGACCACTGTTAAAGAAC 499
DB 576 CTCTGAAGAGAGCTACCGTATCACTTACCGCTTACCACTTCAACACGGGAAGGCA 635
QY 500 GGTGAACCTGGGAGATAGCAACATTCGGCCATTTGAGTTTTCATGTCAGTATGTCG 559
DB 636 GGTCAACCTTGGGACTCCAAATGTCGTCACCTTGAAGTCTTCAATGTCAGTGTTCG 655
QY 560 CAAAATGGGATACGATGAGTTCAGTGTGATGACCCAGTACATCAAGT 609
DB 696 CAAAGTGGGCTACGATGATGTTTCAAGTGGGTCTCCAGTACATCAAGT 745
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RESULT 7

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US-10-425-115-14342
; Sequence 14342, Application US/10425115
; Publication No. US200400214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 14342
; LENGTH: 1221
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_62205C.1
US-10-425-115-14342
```

Query Match 51.0%; Score 340.4; DB 8; Length 1221;
Best Local Similarity 74.7%; Pred. No. 1e-106;
Matches 441; Conservative 0; Mismatches 146; Indels 3; Gaps 1;

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QY 23 GGCTGTACCAATGTTCTTGTAGATGTTTACGGCTTCTTGCAGCATAGGGCTGTG 82
DB 229 GGTGGGGAAGATGTTCTCTGGGACTGGTCTACGGGGTGTGGCTCCCTCGGCTGTG 288
QY 83 GCAGAGGAGGCAAAATCTGTTTCTGGGTCTGCAGATGCTGGCAAGACTACTTCT 142
DB 289 GCAGAGGAGGCAAAATCTCTTCTTGGCTCGACAAAGCGGCAAGACAGCTGCT 348
QY 143 GCACATGCTCAAGATGAGAACTGGGGCAACATCAACGACGATTCACAGTCA 202
DB 349 CCACATGCTCAAGACGAGCGGTTGTGACACACGACGACGACGACGACGACG 408
QY 203 GGAATTAAGTATCAACAGATGAGATTCGAAGATTCGATCGGTGGCCACAAATCG 262
DB 409 GGAAGTCAAGATCGCAAGATCAAGTTCAGAGGTTGACCTCGGCGCCACAGATCG 468
QY 263 TCGAAGCGGTGAGAGGACTATGCTAAGTGTGATGCTATAGTATCTCGTCAAGC 322
DB 469 GCGCCCGTGTGAGAGGATTAACGCAAGGTTGATGCTGTAGTATCACTGGTAGATGC 528
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Oy	323	AGTAGACGGGAGATAATTGGCAGTCACAAGAAGAGCGTGAATTCCTCTCCGCGACA	382
Db	529	ATATGATTAAGAGCCAAATTTGTCTGAATCAAAAGAAAGAGCTCGAATGCTCTCTGTCTGATGA	588
Oy	383	TTCTCTGTCCCAAAGTTCTCTGTGCTGTGCTCTCGGGAAAACAAGTTGATATCCCGTACGCTTC	442
Db	589	TTCCTTGGCCCAATGTTCATTTCTCATCTCTTG6CAACAAAGATTGATATGCCAATATGCTGC	648
Oy	443	TTCTGAAGACGAGTTGCCGTTTCACACTTGGGTTGACCA--TGACCATGTGTAAAGAAAC	499
Db	649	CTCTGAAGAGGAGCTACCGGATACCTTAGCGCTTGTGCACTTCACAAACGGGAAAGGSCAA	708
Oy	500	GGTGAACCTTGGGAGATAGCAACATTCGCGCCCATTTAGAGTTTCAATGTGAAGATTTGTGG	559
Db	709	GGTCAACCTTTGGCGAGCTCCAATGTCCGTCACCTTAGGATCTTCATATGTGAAGTTGTTCG	768
Oy	560	CAAAATGGGGTACGSGTGAAGTTTCAAGTGAAGTGAACCCAGTACATCAAGT 609	
Db	769	CBAATGGGCTACGSGTGAAGTTTCAAGTGAAGTGAACCCAGTACATCAAGT 818	

RESULT 8
US-10-425-115-143343
; Sequence 143343, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 143343
; LENGTH: 1645
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_62206C.1
US-10-425-115-143343

Query Match	51.0%; Score 340.4; DB 8; Length 1645;
Best Local Similarity	74.7%; Pred. No. 1,-106;
Matches 441; Conservative 0; Mismatches 146; Indels 3; Gaps 1;	

Oy	23	GGCTGTACATGTTCTTGTGATGTTGTTTACGCGCTTCTTTCGACATAGAGGCTGTG	82
Db	336	GGTGGGGAGATGTTCTCTGGGACGTGTTACGCGGCTGTGGCCCTCGGCTGTG	395
Oy	83	GCAGAAAGGAGCCAAATCTGTTTCTGGGTCCGACANCTGGGGAAGCTACTCTCT	142
Db	396	GCAGAAAGGAGCCAAAGATCTCTCTTGTGCTCGAACGCGGGAAGACAGCGCTGCT	455
Oy	143	GCACATGTCTCAAGATGAGAAACTGGGGCAACATCAACACGACATATCCAGTCTGAG	202
Db	456	CCACATGTCTCAAGACAGACGAGCGGTGTGACGACACGACGACGACACCCGACGTCGGA	515
Oy	203	GGAGTTGAGTATCAACAGAGTGAAGTTCAAGACATTCGATCTGGGTGGCCACAAATCGC	262
Db	516	GGAGTCAAGCATTCGCGAMATCAAGTTCAAGGCTTCGACCTTCGGGGCCACACGATTCGC	575
Oy	263	TGAGCGCGTGTGAAGGACCTACATGCTTGAAGTGAAGTGAATGATATCGTCAAGCG	322
Db	576	GCGCGCGTGTGAAGGATTACTACGCAAAAGTTGATGCTGATGATACCTGGTAGATGC	635
Oy	323	AGTAGACAGGAGAGATTTGTCTGAGTCAAAAGAAAGCTGATTTCTTCTCCGACGA	382
Db	636	AATATGATTAAGAGCGAATTTGTCTGAATCAAAAGAAAGAGCTGAGTCTCTCTGTATGA	695
Oy	383	TTCTCTGTCCCAAAGTTCTCTGTGCTGTGCTCTCGGGAAAACAAGTTGATATCCCGTACGCTTC	442

D	b		696	TTCTTGGCCAAATTCATTCTTCATCCTTGCGCAACAAGATGATATCCCATGTGC	755
Oy		443	TTCTGAAGACGATTTGCCGTTCAACCTTGGSTGACCA---TGACCATCTGTAAAGAAC	499	
D	b	756	CTGTGAAGAGACTACGGGTATCACCTTAGCGCTTAAGCAAATTCACAAACCGGAGGCGAA	815	
Oy		500	GGTGAACCTTGGGAATAGCAACATTCGGCCCATTGAGTTTTTCATGTCAGATTTGTGCG	559	
D	b	816	GGTCAACCTTGGCCACTCCAAATGTCCGCCACTTGAGGATCTTCAATGTGAGTGTGTTGG	875	
Oy		560	CAAAATGGGGGTACGGTGAAGGTTTCCAAGTGTGATGACCCAGTACATCAAGT	609	
D	b	876	CNAATGGGCTACGGTATGAGTTTCAGTGGGTCTCCCAGTACATCAAGT	925	
 RESULT 9 US-10-425-115-98353 ; Sequence 98353, Application US/10425115 ; Publication NO. US20040214272A1 ; GENERAL INFORMATION: ; APPLICANT: La Rosa, Thomas J. ; APPLICANT: Kovalic, David K. ; APPLICANT: Zhou, Yihua ; APPLICANT: Cao, Yongwei; ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With ; FILE REFERENCE: 38-21(53222)B ; CURRENT APPLICATION NUMBER: US/10/425,115 ; CURRENT FILING DATE: 2003-04-28 ; NUMBER OF SEQ ID NOS: 369326 ; SEQ ID NO 98353 ; LENGTH: 1070 ; TYPE: DNA ; ORGANISM: Zea mays ; FEATURE: ; OTHER INFORMATION: Clone ID: MRT4577_21208C.1 US-10-425-115-98353					
			Query Match	50.7%; Score 338.4; DB 8; Length 1070;	
			Best Local Similarity	74.2%; Pred.No. 4.7e-106;	
			Matches 442; Conservative	0; Mismatches 151; Indels 3; Gaps 1;	
Oy		19	CCAAAGCTGTACCATGTTCTCTGTAGATTTGTTTAGCGCTTCTTGCGACATAGGCG	78	
D	b	169	CCGAGTTGTAAAGTGTCTCTGTGGAAGCTGGTTCTATGAGGGTGTCTGGCATGCTTGGGC	228	
Oy		79	TGTGGCAGAAGAGGCCAAATAATCCGTTTCTGGGCTGTGACAAATGTGCGAAGACTACTC	138	
D	b	229	TGTGGCAGAAGAGGCTAAAGATCCTTCTCTTGGCCTTGACAAAGCCGCGAACACACCC	288	
Oy		139	TTCTGCACATCTCAAGAGTGAAGAATCGGGCAACATCAACAAACGAGTATCCAAAGT	198	
D	b	289	TCTTTCATCTCTGAAGGACGAGCGGCTGTATACAGACACAGCGAGCGATCCCCAGT	348	
Oy		199	CAGAGAGTTAGTATCAACAGAGTGAAGTTCAANGACTTCGATCTGGTGCCACACAA	258	
D	b	349	CAGAAAGTTAGATCCGACAGGATCAAGTTCAAGCGCTTCCACTTGGGGGCCACAGAA	408	
Oy		259	TTCGTCAGCGGTGTGAGGGAAGTATAGTAAAGTGAATGCTATAGTATCTGTGTG	318	
D	b	409	TGCGCCGCGGCTGTGGAAGACTACAGCCAAAGGTGATGCTGTGTACTTGTGG	468	
Oy		319	ACGAGTAGACAGGAGAGATTTGTCTGAGTCAAAAAGAGCTCGATTCCTTCTCCG	378	
D	b	469	ATGCTGTGAACAGGACGTTTTCGAGTGSAAABAAGAGTTGATGTGCTTCTTGAG	528	
Oy		379	ACGATTTCTGTCTCCAGTTCTCTGTGTGTGCTGTGGAAAAACAAGTTGATATCCGTACG	438	
D	b	529	ATGACTCCCTTGCAAAACGTTCTTCTTCATATCTGGGCAACAAGATTGACATCCCAATAG	588	
Oy		439	CTTCTTGAAGACGAGTTGGGGTTCACACTTGGGGTTGACCA--TGACCATCTGGAAG	495	

Db 589 CGGCTTGAAGAGAGAGCTGGCTACTACCTTGGCTGAGCACTTCAACGGGGAAG 648
Qy 496 GAACGGTGAACCTGGGAGATAGCAACATTCGCCCATTTGAGTTTTCATGTGAGTATTTG 555
Db 649 GCAACGTGAACCTTGGCTGATTCGAATGTGGCCCCCTGGAGATCTTCATGTGAGTGTGG 708
Qy 556 TGGCCAAAATGGGGTACGGTGAAGTTTCAAGTGGATGACCCAGTATCAATGGA 611
Db 709 TGGCAGATGGGCTATGTGAAAGCTTCAATGATGTCTCAGTACATCAAGTGA 764

RESULT 10

US-10-425-114-21639
; Sequence 21639, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 21639
; LENGTH: 955
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3354-056-D12_FLI
US-10-425-114-21639

Query Match 50.3%; Score 335.6; DB 7; Length 955;

Best Local Similarity 73.7%; Pred. No. 4,1e-105;

Matches 441; Conservative 0; Mismatches 154; Indels 3; Gaps 1;

Qy 19 CCAAGGCTGTACATGTTCTTGTAGATTGGTTTACGGCTTCTTGGAGCATAGAGG 78
Db 84 CCGAGTTGTAAAGATGTTCTTGGTGAATGTTCTATGGGTTCTGATCGCTTGGGC 143
Qy 79 TGTGGCAGAAAGAGAGCCAAATCCTGTTTCTGGGTTCTGCAATGTGGCAAGTATC 138
Db 144 TGTGGCAGAAAGAGAGCTAAGATCTCTTCTTGGCTTGAACAAGCCGGAAGCAACC 203
Qy 139 TTCTGCACATGCTCAAGATAGAAAATGGGGCAACATCAACGAGTATCAACGT 198
Db 204 TCTTCCACATGCTCAAGAGCAGCGGCTCTTACAGCACAGCCAAACGATGCCACGT 263
Qy 199 CAGAGAGTTGAGTATCAACAGAGTGAAGTTCAAGAGATTCGATCTGGTGGCCACAA 258
Db 264 CAGAGAGTTGAGTATCGAGATCAAGATCAAGGCTTGAACCTTGGGGCCACAGA 323
Qy 259 TCGCTGAGCGGTGTGAGAGGACTACTATGCTAAGTGGATGCTATAGTATCTCGTC 318
Db 324 TCGCCCGCGGCTGTGAGAGGACTACTAGCCAAAGTTGATGCTGTGTGACTTGGTGG 383
Qy 319 ACGCAGTAGACAGGAGAGATTTGCTGAGTCAAAAGAAAGAGCTGATTTCTTCTCCG 378
Db 384 ATGCTGTGACAAAGAGATTTTGGCCGAGTGAAGAGAGAGCTGATGCCCTTCTTCAG 443
Qy 379 ACGATTTCTGTCTCCCAAGTTCTGTGCTGCTCTGGGAAACAAGATTGATATCCCGTAC 438
Db 444 ATGACTCCCTTGAACAAGCTTCTTCTCAATATGGGCAACAAGATTGACATCCCAACG 503
Qy 439 CTTCTTCTGAAGACGAGTTGGGTTTCACTTGGGTTGACCA--TGAACAATGGTAAAG 495
Db 504 CGGCTTCAAGAGAGAGAGTGAAGTACTACTCTCGGCTGTGACAACTTCAACCGGGAAG 563
Qy 496 GAACGGTGAACCTGGGAGATAGCAACATTCGGCCCATTTGAGTTTCAATGTGACGATATG 555

Db 564 GCAACGTGAACCTTGGCGGACTCCAACTCGCCCCCTGGAGATCTTCAATGTGAGTGTGG 623
Qy 556 TGGCCAAAATGGGGTACGGTGAAGTTTCAAGTGGATGACCCAGTATCAATGATTT 613
Db 624 TGGCAGATGGGCTATGTGAAAGGCTTCAATGATGTCTCAGTACATCAAGTGA 681

RESULT 11

US-10-425-114-13536
; Sequence 13536, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 13536
; LENGTH: 966
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB143-001-F4_FLI
US-10-425-114-13536

Query Match 49.8%; Score 332.4; DB 7; Length 966;

Best Local Similarity 73.4%; Pred. No. 5,4e-104;

Matches 439; Conservative 0; Mismatches 156; Indels 3; Gaps 1;

Qy 19 CCAAGGCTGTACATGTTCTTGTAGATTGGTTTACGGCTTCTTGGAGCATAGAGG 78
Db 116 CCGAGTTGTAAAGATGTTCTTGGTGAATGTTCTATGGGTTCTGATCGCTTGGGC 175
Qy 79 TGTGGCAGAAAGAGAGCCAAATCCTGTTTCTGGGTTCTGCAATGTGGCAAGTATC 138
Db 176 TGTGGCAGAAAGAGAGCTAAGATCTCTTCTTGGCTTGAACAAGCCGGAAGCAACC 225
Qy 139 TTCTGCACATGCTCAAGATAGAAAATGGGGCAACATCAACGAGTATCAACGT 198
Db 236 TCTTCCACATGCTCAAGAGCAGAGCGGCTCTTACAGCACAGCCGAGAGTATCCACGT 255
Qy 199 CAGAGAGTTGAGTATCAACAGAGTGAAGTTCAAGAGATTCGATCTGGTGGCCACAA 258
Db 296 CAGAGAGTTGAGTATCGGAGATCAAGATCAAGGCTTGAACCTTGGGGGCCACAGA 355
Qy 259 TCGCTGAGCGGTGTGAGAGGACTACTATGCTAAGTGGATGCTATAGTATCTCGTC 318
Db 356 TCGCCCGCGGCTGTGAGAGGACTACTAGCCAAAGTTGATGTGTGTACTTGGTGG 415
Qy 319 ACGCAGTAGACAGGAGAGATTTGCTGAGTCAAAAGAAAGAGCTGATTTCTTCTCCG 378
Db 416 ATGCTGTGACAAAGAGATTTTGGCCGAGTGAAGAGAGAGCTTGAATGCCCTTTCAG 475
Qy 379 ACGATTTCTGTCTCCAAAGTTCTGTGCTGCTCTTGGGAAAACAAGATTGATATCCCGTAC 438
Db 476 ATGACTCCCTTGAACAAGCTTCTTCTCAATATGGGCAACAAGATTGACATCCCAACG 535
Qy 439 CTTCTTCTGAAGACGAGTTGGGTTTCACTTGGGTTGACCA--TGAACAATGGTAAAG 495
Db 536 CGGCTTCAAGAGAGAGAGTGAAGTACTACTCTCGGCTGTGACAACTTCAACCGGGAAG 595
Qy 496 GAACGGTGAACCTGGGAGATAGCAACATTCGGCCCATTTGAGTTTCAATGTGACGATATG 555
Db 596 GCAACGTGAACCTTGGCGGACTCCAAATGTCCGGCCCTTGGAGATCTTCAATGTGAGTGTGG 655

Qy 556 TGGCAAAATGGGGTACGGTGAAGTTCAGTGAAGCCAGTACATCAAGTATT 613
Db 656 TGGCAAGATGGGCTATGGGGAAGGCTTCAATGATGTCTGATCATCAAGTGAAT 713

RESULT 12
US-10-425-114-33380
; Sequence 33380, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaka, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 33380
; LENGTH: 1017
; TYPE: DNA
; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: UC-ZMFLM01703E09_FLI
US-10-425-114-33380

Query Match 49.8%; Score 332.4; DB 7; Length 1017;
Best Local Similarity 73.4%; Pred. No. 5,5e-104;

Matches 439; Conservative 0; Mismatches 156; Indels 3; Gaps 1;

Qy 19 CCAAGGCTGTACATGTTCTTGTAGATTGTTTACGGCTTCTTGAGCATAGGCG 78
Db 97 CCGAGTTGTAAGATGTTCTGTGTGACTGTTCTATGGGGTGTGGCATCGCTTGGCG 156
Qy 79 TGTGGCAAGAGAGGCCAAATCTCTGTTTGTGGGTCTCGCATGCTGGGAAGATCTC 138
Db 157 TGTGGCAAGAGAGGCTAAGATCTCTTCTTGGCCCTGCAACGCGCGGCAAGACCC 216
Qy 139 TTCTGCACATGCTCAAGATGAGAACTGGGGCAATCAACCAAGTATCCAACT 198
Db 217 TCTTCAATGCTGAAGAGAGAGCGGCTCTGACGACCAAGCGAGCATACCCAGT 276
Qy 199 CAGAGAGTTGATATCAACAGATGAAGTTCAAGGATTCGATCTGGGTGGCACAA 258
Db 277 CAGAAAGTTGACATCGCAGAGATCAAGTTCAAGGCTTCGACTTGGGGGCAACAGA 336
Qy 259 TCGCTGACGCGTGTGAGGAGCTACTATGCTAAGGTGATGCTATAGTATCTGCTG 318
Db 337 TCGCCGCGCGTCTGGAAGACTACTACGCCAAGGTTGATGCTGTGTACTTGGTGG 396
Qy 319 AGCAGTAGACAGAGGAGATTGCTGAGTCAAGAAAGAGCTCGATCTCTCTCCG 378
Db 397 ATCTGTTGACAAAGAACTTTTGGAGTGAAGAGAGCTTGAAGCTCTTCTTTCAG 456
Qy 379 ACGATTCTGTCCTCCAAAGTCTGTGCTCTCTGAGAAACAAGATTGATATCCGTACG 438
Db 457 ATGACTCTCTTGAAGAGTCTTCTTCTCATACCTGGGCAACAGATTGACATCCATACG 516
Qy 439 CTTCTTCTGAAGACGAGTTGCGGTTCACTTGGGTGACCA--TGACCACTGGTAAAG 495
Db 517 CCGCTTCAAGAGAGAGAGCTGAGTACTACCTCGGCTGAGCAACTTCAACACGGGAAG 576
Qy 496 GAACGTTGAACCTGGAGATAGCAACATGGGCCATTGAGGTTTTCATGAGCATATTG 555
Db 577 GCAACGTGAACCTGGCGACTCCAGATCGGCGCCCTGAGATCTTATGAGCATGTTGG 636
Qy 556 TGGCAAAATGGGGTACGGTGAAGTTCAGTGAAGCCAGTACATCAAGTATT 613
Db 637 TGGCAAGATGGGCTATGGGGAAGGCTTCAATGATGTCTGATCATCAAGTGAAT 694

RESULT 13
US-10-425-115-98354
; Sequence 98354, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 98354
; LENGTH: 1334
; TYPE: DNA
; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: MRT4577_21209C.1
US-10-425-115-98354

Query Match 49.8%; Score 332.4; DB 8; Length 1334;
Best Local Similarity 73.4%; Pred. No. 6,4e-104;

Matches 439; Conservative 0; Mismatches 156; Indels 3; Gaps 1;

Qy 19 CCAAGGCTGTACATGTTCTTGTAGATTGTTTACGGCTTCTTGAGCATAGGCG 78
Db 257 CCGAGTTGTAAGATGTTCTGTGTGACTGTTCTATGGGGTGTGGCATCGCTTGGCG 316
Qy 79 TGTGGCAAGAGAGGCCAAATCTCTGTTTGTGGGTCTCGCATGCTGGGAAGATCTC 138
Db 317 TGTGGCAAGAGAGGCTAAGATCTCTTCTTGGCCCTGCAACGCGCGGCAAGACCC 376
Qy 139 TTCTGCACATGCTCAAGATGAGAACTGGGGCAATCAACCAAGTATCCAACT 198
Db 377 TCTTCAATGCTGAAGAGAGAGCGGCTCTGACGACCAAGCGAGCATACCCAGT 436
Qy 199 CAGAGAGTTGATATCAACAGATGAAGTTCAAGGATTCGATCTGGGTGGCACAA 258
Db 437 CAGAAAGTTGACATCGCAGAGATCAAGTTCAAGGCTTCGACTTGGGGGCAACAGA 496
Qy 259 TCGCTGACGCGTGTGAGGAGCTACTATGCTAAGGTGATGCTATAGTATCTGCTG 318
Db 497 TCGCCGCGCGTCTGGAAGACTACTACGCCAAGGTTGATGCTGTGTACTTGGTGG 556
Qy 319 AGCAGTAGACAGAGGAGATTGCTGAGTCAAGAAAGAGCTCGATCTCTCTCCG 378
Db 557 ATCTGTTGACAAAGAACTTTTGGAGTGAAGAGAGCTTGAAGCTCTTCTTTCAG 616
Qy 379 ACGATTCTGTCCTCCAAAGTCTGTGCTCTCTGAGAAACAAGATTGATATCCGTACG 438
Db 617 ATGACTCTCTTGAAGAGTCTTCTTCTCATACCTGGGCAACAGATTGACATCCATACG 676
Qy 439 CTTCTTCTGAAGACGAGTTGCGGTTCACTTGGGTGACCA--TGACCACTGGTAAAG 495
Db 677 CCGCTTCAAGAGAGAGAGCTGAGTACTACCTCGGCTGAGCAACTTCAACACGGGAAG 736
Qy 496 GAACGTTGAACCTGGAGATAGCAACATGGGCCATTGAGGTTTTCATGAGCATATTG 555
Db 737 GCAACGTGAACCTGGCGACTCCAGATCGGCGCCCTGAGATCTTATGAGCATGTTGG 796
Qy 556 TGGCAAAATGGGGTACGGTGAAGTTCAGTGAAGCCAGTACATCAAGTATT 613
Db 797 TGGCAAGATGGGCTATGGGGAAGGCTTCAATGATGTCTGATCATCAAGTGAAT 854

RESULT 14
US-10-425-114-20345
; Sequence 20345, Application US/10425114

Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 20345
LENGTH: 966
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB3180-039-D5_FLI
US-10-425-114-20345

Query Match 49.5%; Score 330.4; DB 7; Length 966;

Best Local Similarity 74.3%; Pred. No. 2.7e-103; Indels 3; Gaps 1;

Matches 431; Conservative 0; Mismatches 146;

33 ATGTTCTTGATGATGTTTACGGCTTTCTTGCAGCATAGGGCTGTGGCAGAGAG 92
130 ATGTTCTTGATGATGTTTACGGCTTTCTTGCAGCATAGGGCTGTGGCAGAGAG 189
93 GCCAAATCTGTTCTGAGTCTGACATGCTGGCAAGACTCTTCTGACATGCTC 152
190 GCGAAGATCTCTCTCTGAGCTGACACACCGCGCAAGACACAGCTGCTCAATCTC 249
153 AAGATGAGAACTGGGCGCAATCAACCAAGCATATCCAGTACAGAGAGTTAGT 212
250 AAGACGAGCGGTGTGACACACCGCGCAAGCATATCCAGTACAGAGAGTTAGT 309
213 ATCAACAGATGAGTTCAAGATTCGATCTGGGTGGCCACACATTCGCTGACGCTG 272
310 ATCGCAAGATCAAGTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCA 369
273 TGGAGGACTACTATGCTAAGTGTGATGATGATGATGATGATGATGATGATGAT 332
370 TGGAGGACTACTATGCTAAGTGTGATGATGATGATGATGATGATGATGATGAT 429
333 GAGGATTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 392
430 GAGGATTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 489
393 CAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 452
490 AATGTTCCATTTCTCATCTTGGCAACAGATGATGATGATGATGATGATGATGAT 549
453 GAGTTCGCTTCACTTGGGTGACCA--TGACCACTGTTAAAGAACGTTGACCTG 509
550 GAGTTCGCTTCACTTGGGTGACCA--TGACCACTGTTAAAGAACGTTGACCTG 609
510 GGAATAGCAATTCGCGCCATTTGAGTTTCAATGTCATATTTGCGGCAAAATGGG 569
610 GCGCATCTCAATGTCGCGCCATTTGAGTTTCAATGTCATATTTGCGGCAAAATGGG 669
570 TACGGTGAAGTTTCAAGTGAATGACCAATGATCAAGT 609
670 TACGGTGAAGTTTCAAGTGAATGACCAATGATCAAGT 709

RESULT 15

US-10-425-114-20291

Sequence 20291, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jindong

APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 20291
LENGTH: 1051
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB3180-021-F8_FLI
US-10-425-114-20291

Query Match 49.5%; Score 330.4; DB 7; Length 1051;

Best Local Similarity 74.3%; Pred. No. 2.8e-103;

Matches 431; Conservative 0; Mismatches 146; Indels 3; Gaps 1;

33 ATGTTCTTGATGATGTTTACGGCTTTCTTGCAGCATAGGGCTGTGGCAGAGAG 92
155 ATGTTCTTGATGATGTTTACGGCTTTCTTGCAGCATAGGGCTGTGGCAGAGAG 214
93 GCCAAATCTGTTCTGAGTCTGACATGCTGGCAAGACTCTTCTGACATGCTC 152
215 GCGAAGATCTCTCTCTGAGCTGACACACCGCGCAAGACACAGCTGCTCAATCTC 274
153 AAGATGAGAACTGGGCGCAATCAACCAAGCATATCCAGTACAGAGAGTTAGT 212
275 AAGACGAGCGGTGTGACACACCGCGCAAGCATATCCAGTACAGAGAGTTAGT 334
213 ATCAACAGATGAGTTCAAGATTCGATCTGGGTGGCCACACATTCGCTGACGCTG 272
335 ATCGCAAGATCAAGTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCA 394
273 TGGAGGACTACTATGCTAAGTGTGATGATGATGATGATGATGATGATGATGAT 332
395 TGGAGGACTACTATGCTAAGTGTGATGATGATGATGATGATGATGATGATGAT 454
333 GAGGATTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 392
455 GAGGATTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 514
393 CAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 452
515 AATGTTCCATTTCTCATCTTGGCAACAGATGATGATGATGATGATGATGATGAT 574
453 GAGTTCGCTTCACTTGGGTGACCA--TGACCACTGTTAAAGAACGTTGACCTG 509
575 GAGTTCGCTTCACTTGGGTGACCA--TGACCACTGTTAAAGAACGTTGACCTG 634
510 GGAATAGCAATTCGCGCCATTTGAGTTTCAATGTCATATTTGCGGCAAAATGGG 569
635 GCGCATCTCAATGTCGCGCCATTTGAGTTTCAATGTCATATTTGCGGCAAAATGGG 694
570 TACGGTGAAGTTTCAAGTGAATGACCAATGATCAAGT 609
695 TACGGTGAAGTTTCAAGTGAATGACCAATGATCAAGT 734

Search completed: December 9, 2005, 01:28:19

Job time : 800 secs

Qy	205	AGTGAAGTATCAACAG---AGTGAAGTTCAAAAGCAATTGAGTCTGGATGGCCACACAAATCG	261
Db	484	CTGTGAAAGCTCCTGGGACAGTGTACTACTCTCTCTGGGACGTTGGGGGGGAGAGCCCCG	543
Qy	262	CTGCAGCGCTGTGGAGGAGCTACTATGCTAAAGTGGATGCTATAGTATCTGTGCACG	321
Db	544	TCAGAGCCAGCTGGAAAGACTATCTGGAAAGGCACAGATATCCTCGTACGCTGTGCACA	603
Qy	322	CAGTAGACAGGAGAAATTGCTGAGTCAAAAGAAAGACTCGATTCTTTCTTCGACG	381
Db	604	GCAACAGTGAAGCCCGCTTACCCGATCGGCGGCTGAGCTCACAGAACTCTGAAACGAC	663
Qy	382	ATTCTCTGATCCCAAGTTCTCTGCTGCTGCTCTGGGAAAAGAAATTGATATCCCGTACG	439
Db	664	CCAACTAGTGTGGCGTCCCTTCTTGATGCTGTGGCAACAGACGAGGACCTGATGCG	721

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RESULT 8
US-10-750-185-28179
; Sequence 28179, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: Denise, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28179
; LENGTH: 676
; TYPE: DNA
; ORGANISM: Bovine 19866880693146
US-10-750-185-28179

```

Query Match	5.5%	Score 36.8	DB 6	Length 676
Best Local Similarity	61.5%	Pred. No. 0.0072		
Matches	59	Conservative	0	Mismatches 37
				Indels 0
				Gaps 0
OY	89	GGAGGCCAAATCCGTTTCGGGCTGGACATCTGGCAGAGCTACTCTCTGCACAT	148	
Db	404	GGAGGCCAGGTGTGATGATGAGGCGCTGGACTGGGCGGCAAGCACGCTCTGTACA	463	
OY	149	GCTCAAGATGAGAAACTGGGGCAATCAACCAAC	184	
Db	464	ACTGAAGGGCCACCAAGCTGATGAGAACCTTGCCAC	499	

RESULT 9
US-10-750-185-46137
Sequence 46137, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM11100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US60/437,482

```

? PRIOR FILING DATE: 2002-12-31
? NUMBER OF SEQ ID NOS: 64922
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO: 46137
? LENGTH: 976
? TYPE: DNA
? ORGANISM: Bovine
US-10-750-185--46137 19866881259930

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[illegible]

```

RESULT 10
US-10-750-185-58595
? Sequence 58595, Application US/10750185
? Publication No. US20050260603A1
? GENERAL INFORMATION:
? APPLICANT: MMI GENOMICS, INC.
? APPLICANT: DENISE, Sue K.
? APPLICANT: KERR, Richard
? APPLICANT: ROSENFELD, David
? APPLICANT: HOLM, Tom
? APPLICANT: BATES, Stephen
? APPLICANT: FAVTIN, Dennis
? TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
? FILE REFERENCE: MM1100-2
? CURRENT APPLICATION NUMBER: US/10/750.185
? CURRENT FILING DATE: 2003-12-31
? PRIOR APPLICATION NUMBER: US 60/437,482
? PRIOR FILING DATE: 2002-12-31
? NUMBER OF SEQ ID NOS: 64922
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 58595
? LENGTH: 1424
? TYPE: DNA
? ORGANISM: Bovine 19866881395308
US-10-750-185-58595

```

Query Match	4.9%;	Score 33;	DB 6;	Length 1424;
Best Local Similarity	47.4%;	Pred. No. 0.25;		
Matches	99;	Conservative	0;	Mismatches 110;
			Indels	0;
			Gaps	0;
QY	150	CTCAAGATGAGAACTGGGGCAACATCAACCAACGAGTATCCAGCTCAGAGAGTTG	209	
DB	950	CTGAGAGTCTCAGAAATGGATTAAACCTPAGAAATGATGTMACTCCACAGCTGAGTCA	1009	
QY	210	AGTATCAACAGAGGAGAGTTCAAAGCAATGCGATGTGGGTGGCCACACATAGCTCGACGC	269	
DB	1010	AATTCAGAAAGGCTAACCCCTTCTGAGCAAGGAAAGGAGATTTTATATCTTCTTAAATT	1069	
QY	270	GTGTGAGAGGACTACTATGTCTAGAGTGATGCTATAGTATCTCGTCGACGCAAGTAAAC	329	
DB	1070	GAAATATGGGCTTAACCTTAATAAATTTGATGTGAAATCGAAATCCAACTACTTTGGGCAC	1129	
QY	330	AGGAGAGATTTCCTGAGCTCAAAAGAAAGA	358	
DB	1130	CTGATGTGTAAGAGCTTAACCTCAATTGGAAAA	1158	

RESULT 11
US-10-750-185-62691/c
; Sequence 62691, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62691
; LENGTH: 1613
; TYPE: DNA
; ORGANISM: Bovine 1986680920645
US-10-750-185-62691

Query Match 4.9%; Score 33; DB 6; Length 1613;
Best Local Similarity 57.1%; Pred. No. 0.27;
Matches 60; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 544 TGTGCAATATTGCGCAAAATGGGTACGTAAGTTTCAAGTGATGACCAAGTACA 603
DB 1065 TGTAAAGTGTGTTGCTTAATTCAGGGCGTGGAGTAGATAGTACAGAAATAGTTCA 1006
QY 604 TCAAGTATTGTTTCTCTGGAAGAGAACTTAGCTCGGTGTT 648
DB 1005 TCAAGTATTGTTTCTCTGGAAGAGAACTTAGCTCGGTGTT 961

RESULT 12
US-10-750-185-38735
; Sequence 38735, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38735
; LENGTH: 1994
; TYPE: DNA
; ORGANISM: Bovine 198668081805084
US-10-750-185-38735

Query Match 4.9%; Score 32.6; DB 6; Length 1994;
Best Local Similarity 51.7%; Pred. No. 0.42;
Matches 74; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 365 TTCTCTTCTCCGACGATTTCTGTCCCAAGTTCTGTCTCTGCTGGAACAAGAT 424
DB 973 TTTATGTTCTTCAAAATAGATCTGTCCACAGATGCTGTGCTTCCCTGCGGCTCAGA 1032

QY 425 TGATATCCGTCAGCTTCTTCTGAAAGACGATTCGCGTTCACTTGAGTGAACATGAC 484
DB 1033 TGTAAAGATCTGCTTGAATGAGGAGTCTTGAAGTTGATCTCCGGTGGGAAGATC 1092
QY 485 CACTGTTAAAGAACGTTGAACC 507
DB 1093 CCTGAGTAGGAAATGCAAAAC 1115

RESULT 13
US-10-750-185-255/c
; Sequence 255, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 255
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Bovine MMBT08970
US-10-750-185-255

Query Match 4.8%; Score 32.2; DB 6; Length 600;
Best Local Similarity 55.2%; Pred. No. 0.29;
Matches 58; Conservative 2; Mismatches 45; Indels 0; Gaps 0;

QY 544 TGTGCAATATTGCGCAAAATGGGTACGTAAGTTTCAAGTGATGACCAAGTACA 603
DB 409 TGTAAAGTGTGTTGCTTAATTCAGGGCGTGGAGTAGATAGTACAGAAATAGTTCA 350
QY 604 TCAAGTATTGTTTCTCTGGAAGAGAACTTAGCTCGGTGTT 648
DB 349 TCAAGTATTGTTTCTCTGGAAGAGAACTTAGCTCGGTGTT 305

RESULT 14
US-10-750-185-47498/c
; Sequence 47498, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47498
; LENGTH: 2140
; TYPE: DNA
; ORGANISM: Bovine 1986680489188
US-10-750-185-47498

Query Match	4.8%	Score 32;	DB 6;	Length 2140;
Best Local Similarity	56.7%;	Pred. No. 0.71;		
Matches 59; Conservative	0;	Mismatches 45;	Indels 0;	Gaps 0;

Dy 33 ATGTTCTTGATAGTGGTTTACCGCTTTCGCAGCATAGGGCTGTGCCAAGAAG 92
 ||| |||| | |||| | |||| | |||| | |||| |
Db 753 AATAATTCAAGGTTGGTAGATGTTATATATAGTATATAGCATGATAGTTGAT 694

QY 93 GCCAAATCCTGTTCTGGGCTCGACATGCTGGCAAGACTAC 136
 Db 693 ACTATAATCCTGATTTTGTCTTATGCCCATAAAAACATGACAAC 6500

RESULT 15

US-10-750-185-40368/c
; Sequence 40368, Application US/10750185
; Publication No. US20050260603A1
CUMULATIVE INDEX

GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.

APPLICANT: DENISE, Sue K.

APPLICANT: KERR, Richard
DOCUMENT ID: 30014

APPLICANT: ROSENFELD, DAVID

APPLICANT:	RATES	ST
HULM, 10M		

APPLICANT: EANTIN Dennis

TITLE OF INVENTION: COMPOSITIONS FOR IMPROVING BOVINE TRAITS

FILE REFERENCE: MMT1100-2

CURRENT APPLICATION NUMBER: US/10/750.185

CURRENT FILING DATE: 2003-12-31

PRIOR APPLICATION NUMBER: US 60/

PRIOR FILING DATE: 2002-12-31

NUMBER OF SEQ ID NOS: 64922

; SOFTWARE: PatentIn version 3.1.1

; SEQ ID NO 40368

; LENGTH: 3279

; TYPE: DNA

ORGANISM:

US-10-750-185-40368

Query Match	4.8%	Score 31.8;	DB 6;	Length 3279;
Best Local Similarity	51.8%	Pred. No. 1.1;		
Matches 72;	Conservative 0;	Mismatches 67;	Indels 0;	Gaps 0;

369 CTTCTCTCCGACGATTTCTGTGCCAAGTCTGTGCTGTGCTCTGGAAACAAGTTGAT 428
Gy
Db 2126 CTTAGCTGCTACAGTCTCACTTCAAAATAGTTTGTACTCCCTTGGTACTCAGAGGCT 206

429 ATCCCGACGCTCTCTGAGACGAGTCCGGTCACACTGGAGTACCATATACCACT 488
 2066 AAGTGTCTGCTGCAATGTGGGAGATCTGGGTTCAATCCTTGGGTTGGGAAGATCCCT 2007

QY	485	GGTAATGGAACTGGTGAAC	507
Db	2006	GGAGAAGGAATGGCAACC	1988

Search completed: December 9, 2005, 01:32:37
Job time : 250 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 9, 2005, 00:07:31 ; Search time 134 Seconds
(without alignments)
629.558 Million cell updates/sec

Title: US-10-688-481-11
Perfect score: 998
Sequence: 1 MFLVDMFYGFRLASIGLMQKE.....SIVRKMGYGEGRFMNTQYIK 192

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378761 residues
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	998	100.0	192	5	ABB81583 Physcomit
2	998	100.0	192	8	ADT91574 Physcomit
3	880.5	88.2	225	8	ADY22898 Plant ful
4	880.5	88.2	229	8	ADY23452 Plant ful
5	880.5	88.2	236	8	ADY05691 Plant ful
6	867.5	86.9	255	8	ADY08914 Plant ful
7	866.5	86.8	193	7	ABM74047 DNA clone
8	862.5	86.4	193	3	AAG30108 Arabidops
9	862.5	86.4	208	8	ABG59985 Human DIT
10	862.5	86.4	208	8	ADX88378 Plant ful
11	862.5	86.4	236	8	ADY07438 Plant ful
12	862.5	86.4	244	8	ADY07420 Plant ful
13	862.5	86.4	251	8	ADX87922 Plant ful
14	862.5	86.4	280	8	ADY10442 Plant ful
15	859.5	86.1	266	8	ADY75842 Plant ful
16	851.5	85.3	191	3	AAG30109 Arabidops
17	850.5	85.2	193	3	AAG15475 Arabidops
18	842.5	84.4	292	3	AAG35214 Zea mays
19	842.5	84.4	300	3	AAG35213 Zea mays
20	842.5	84.4	305	3	AAG35212 Zea mays
21	822.5	82.4	193	3	AAG30994 Arabidops
22	674.5	67.6	193	4	ABB62939 Drosophila
23	671.5	67.3	155	3	AAG30110 Arabidops
24	660.5	66.2	155	3	AAG15476 Arabidops

25	649.5	65.1	155	3	AAG30995 Arabidops
26	627	62.8	189	6	ABJ25768 Apepexg11
27	615	61.6	189	6	ABJ26368 Apepexg11
28	615	61.6	199	9	ADY64776 S. mansoni
29	614.5	61.6	198	2	AAW77416 Human GTP
30	614.5	61.6	198	3	AAW77416 Human GTP
31	614.5	61.6	198	4	AAW77416 Human SAR
32	614.5	61.6	198	4	AAW77416 Chinese h
33	614.5	61.6	198	8	ADY020049 Human PRO
34	614.5	61.6	198	8	ADY020049 Human PRO
35	614.5	61.6	198	8	ADY24917 PRO polyp
36	614.5	61.6	199	2	AAW74864 Human sec
37	614.5	61.6	199	2	AAW74864 Human nov
38	614.5	61.6	199	6	ABO34509 Region of
39	614.5	61.6	199	7	ADY23170 Novel hum
40	614.5	61.6	199	8	ADH74172 Human sec
41	613.5	61.5	190	5	ABP73936 Candida a
42	606.5	60.8	190	4	ABG70914 S cerevis
43	605.5	60.7	198	8	ADY032522 Sar1b GTP
44	600.5	60.2	198	8	ADY032526 Mutant Sa
45	600.5	60.2	198	8	ADY032530 Mutant Sa

ALIGNMENTS

RESULT 1
ABB81583
ID ABB81583 standard; protein; 192 AA.
XX
AC ABB81583;
XX
DT 18-SEP-2002 (first entry)
XX
DE Physcomitrella patens GBP-1 protein sequence SEQ ID NO:11.
XX
XX Physcomitrella patens; GBP; GTP binding protein; GBSRP; plant;
XX GTP binding stress-related protein; transgenic plant; agricultural;
XX environmental stress; salinity; drought; temperature.
XX
XX Physcomitrella patens.
XX
OS US2002066124-A1.
XX
PN 30-MAY-2002.
PD
PF 06-APR-2001; 2001US-00828310.
XX
PR 07-APR-2000; 2000US-0196001P.
XX
XX (SILV/) SILVA O D C E.
XX (BOHN/) BOHNERT H J.
XX (THIE/) THIELEN N V.
XX (CHEN/) CHEN R.
PI Silva ODCE, Bohnert HJ, Thielen NV, Chen R;
XX WPI; 2002-556781/59.
DR N-PSDB; ABN69814.
XX
XX Novel GTP binding stress-related proteins and genes encoding the
XX proteins, useful for producing transgenic plants having increased
XX tolerance to environmental stress as compared to wild type variety of
XX plant cell.
XX
XX Claim 14; Fig 3A; 73p; English.
XX
XX The present invention describes an isolated GTP binding stress-related
XX protein (GBSRP) (I) from Physcomitrella patens, selected from GTP binding
XX protein-1 (GBP-1), GBP-2, GBP-3, GBP-4 and GBP-5, or its orthologues. (I)
XX can be used for producing a transgenic plant (e.g. maize, wheat, rice,
XX oat, triticale, rice, barley, soybean, peanut, cotton, rapeseed, canola,
XX manihot, pepper, sunflower, tagetes, solanaceous plants, potato, tobacco,

CC eggplant, tomato, vicia species, pea, alfalfa, coffee, cacao, tea, Salix
CC species, oil palm, coconut, perennial grass and forage crops). The
CC transgenic plants produced have increased tolerance to environmental
CC stress (e.g. salinity, drought and temperature) as compared to a wild
CC type variety of the plant, from the plant cell. GBSRP polynucleotide
CC sequences can be used as markers for specific regions of the genome, and
CC also in functional studies of P. patens proteins. They can also be used
CC for evolutionary studies and protein structural studies. The present sequence
CC represents the P. patens GBP-1 protein, which is used in the
CC exemplification of the present invention

XX Sequence 192 AA;

Query Match 100.0%; Score 998; DB 5; Length 192;

Best Local Similarity 100.0%; Pred. No. 1.4e-106;
Matches 192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFLVDMFYGFGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGQHOPQPTSEELS 60
DB 1 MFLVDMFYGFGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGQHOPQPTSEELS 60
QY 61 INRVKFAFDLGGHTTARRVWRDYYAKVDALVYLVDVDRERFAESKKEIDSLSDSL 120
DB 61 INRVKFAFDLGGHTTARRVWRDYYAKVDALVYLVDVDRERFAESKKEIDSLSDSL 120
QY 121 QVPVLVGNKIDIPYASSEDELRFLLGLTMTTGKGVNLGDSNIRPIEVFMCISIVRMGY 180
DB 121 QVPVLVGNKIDIPYASSEDELRFLLGLTMTTGKGVNLGDSNIRPIEVFMCISIVRMGY 180
QY 181 GEGFKMNTQYIK 192
DB 181 GEGFKMNTQYIK 192

RESULT 2

ID ADT91574 standard; protein; 192 AA.

XX ADT91574;

DT 16-DEC-2004 (first entry)

XX Physcomitrella patens GTP binding protein, PGBP-1.

DE GTP-binding stress-related protein; GBSRP; transgenic plant;

KM environmental stress tolerance; stress resistance; cell metabolism;

XX GTP binding protein; GBP.

OS Physcomitrella patens.

XX US2004194163-A1.

PN 30-SEP-2004.

XX 17-OCT-2003; 2003US-00688481.

PR 07-APR-2000; 2000US-0196001P.

PR 06-APR-2001; 2001US-00828310.

XX (BADI) BASF PLANT SCI GMBH.

PI Da Costa E SilvaO, Bohnert HJ, Thieleen NV, Chen R;

XX WPI; 2004-698822/68.

DR N-PSDB; ADT91569.

XX Novel isolated nucleic acid encoding polypeptide e.g., GTP-binding stress

PT -related protein, useful for producing vector utilized for producing

XX transgenic plant that has increased tolerance to environmental stress.

PS Example 6; SEQ ID NO 11; 62pp; English.

XX The invention relates to nucleic acid sequences encoding GTP-binding

CC stress-related proteins (GBSRP). GBSRP DNA is useful for producing a
CC recombinant expression vector utilized for producing a transgenic plant
CC that has increased tolerance to environmental stress, for identifying and
CC Physcomitrella patens and related organisms, for identifying and
CC localising P. patens sequences of interest, for evolutionary studies, for
CC determining GBSRP regions required for function, for modulating GBSRP
CC activity, for modulating metabolism of one or more cell function, for
CC modulating transport of one or more compounds, for modulating stress
CC resistance or as markers for specific regions of the genome of P. patens.
CC The present sequence is the Physcomitrella patens GTP binding protein
CC (GBP).

XX Sequence 192 AA;

Query Match 100.0%; Score 998; DB 8; Length 192;

Best Local Similarity 100.0%; Pred. No. 1.4e-106;
Matches 192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFLVDMFYGFGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGQHOPQPTSEELS 60
DB 1 MFLVDMFYGFGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGQHOPQPTSEELS 60
QY 61 INRVKFAFDLGGHTTARRVWRDYYAKVDALVYLVDVDRERFAESKKEIDSLSDSL 120
DB 61 INRVKFAFDLGGHTTARRVWRDYYAKVDALVYLVDVDRERFAESKKEIDSLSDSL 120
QY 121 QVPVLVGNKIDIPYASSEDELRFLLGLTMTTGKGVNLGDSNIRPIEVFMCISIVRMGY 180
DB 121 QVPVLVGNKIDIPYASSEDELRFLLGLTMTTGKGVNLGDSNIRPIEVFMCISIVRMGY 180
QY 181 GEGFKMNTQYIK 192
DB 181 GEGFKMNTQYIK 192

RESULT 3

ID ADY22898 standard; protein; 225 AA.

XX ADY22898;

DT 21-APR-2005 (first entry)

XX Plant full length insert polypeptide seqid 70682.

DE plant protectant; plant growth regulant; gene therapy; plant;

KM recombinant DNA construct; physical array; plant breeding marker;

KM cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;

KM extreme osmotic condition; pathogen tolerance; pest tolerance;

KM growth rate; cell cycle pathway; disease resistance;

KM galactomannan production; lignin production; plant growth regulator;

KM yield; plant growth; plant development; seed oil; protein yield;

XX protein content.

XX Undifferentiated.

OS US2004034888-A1.

PN 19-FEB-2004.

XX 28-APR-2003; 2003US-00425114.

PR 06-MAY-1999; 99US-00304517.

PR 05-NOV-2001; 2001US-00985676.

XX (LIU/) LIU J.

XX (ZHOU/) ZHOU Y.

XX (KOVA/) KOVALIC D K.

XX (SCRE/) SCREEN S E.

XX (TAB/) TABASKA J E.

XX (CAO/) CAO Y.

XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;

XX WPI; 2004-180133/17.
 DR
 XX
 PT New recombinant DNA construct, useful for improving plant tolerance to
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 PT pests, for conferring increased resistance to plant disease, or for
 PT improving yield.
 XX
 PS Claim 1; SEQ ID NO 70682; 15pp; English.
 XX
 CC The invention describes a recombinant DNA construct comprising a
 CC polynucleotide consisting of a sequence encoding an amino acid sequence
 CC available in electronic form from the US patent office at
 CC ftp.segdata.uspto.gov/sequence.html?docid:2004034888. The polynucleotide
 CC of the invention are also useful in physical arrays of molecules and as
 CC plant breeding markers. The recombinant DNA construct is useful for
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, for conferring
 CC increased resistance to plant disease, for producing galactomannan,
 CC lignin or plant growth regulators, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This is the amino acid sequence of a plant full length insert
 CC polypeptide that can be used in the recombinant DNA construct of the
 CC invention.
 CC
 CC Sequence 225 AA;
 XX
 SQ
 Query Match 88.2%; Score 880.5; DB 8; Length 225;
 Best Local Similarity 84.5%; Pred. No. 6-8e-93;
 Matches 163; Conservative 19; Mismatches 10; Indels 1; Gaps 1;
 QY 1 MFLVDMFYGFGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGQHOPQYPTSEELS 60
 DB 33 MFLVDMFYGVASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEBLVQHOPQYPTSEELS 92
 QY 61 INRVKFAFDLGGHTTARWRDYAKVDAIVLVDAVDRERFAESKEKELSDLSLSDLS 120
 DB 93 IGRIRKFAFDLGGHQAIRRWKDYAKVDAVVLDVAVDERFAESKEKELDALLADSLA 152
 QY 121 QVPLVVGNGKIDIPYASSEDELRTGLT-MTGGKGVNIGDSNIRPIEFVMSIVRKMG 179
 DB 153 NVFPLIGNKIDIPYASSEELRYLGLSNFTGKGNVLADSNVRLPIFMSVVRKMG 212
 QY 180 YGEGFKMMTOYIK 192
 DB 213 YGEGFKMMSQYIK 225
 RESULT 4
 ADY23452
 ID ADY23452 standard; protein; 229 AA.
 AC
 XX ADY23452;
 DT 21-APR-2005 (first entry)
 XX
 DE Plant full length insert polypeptide seqid 71236.
 XX
 KW plant proectant; plant growth regulant; gene therapy; plant;
 KW recombinant DNA construct; physical array; plant breeding marker;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;
 KW growth rate; cell cycle pathway; disease resistance;
 KW galactomannan production; lignin production; plant growth regulator;
 KW yield; plant growth; plant development; seed oil; protein yield;
 KW protein content.
 KW
 XX Undentified.
 OS
 XX

PN US2004034888-A1.
 XX
 XX 19-FEB-2004.
 XX
 XX 28-APR-2003; 2003US-00425114.
 PF
 XX 06-MAY-1999; 99US-00304517.
 PR
 XX 05-NOV-2001; 2001US-00985676.
 XX
 PA (LIU/) LIU J.
 PA (ZHOU/) ZHOU Y.
 PA (KOVA/) KOVALIC D. K.
 PA (SCRE/) SCREEN S. E.
 PA (TABAS/) TABASKA J. E.
 PA (CAO/) CAO Y.
 XX
 PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
 DR
 XX WPI; 2004-180133/17.
 XX
 PT New recombinant DNA construct, useful for improving plant tolerance to
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 PT pests, for conferring increased resistance to plant disease, or for
 PT improving yield.
 XX
 PS Claim 1; SEQ ID NO 71236; 15pp; English.
 XX
 CC The invention describes a recombinant DNA construct comprising a
 CC polynucleotide consisting of a sequence encoding an amino acid sequence
 CC available in electronic form from the US patent office at
 CC ftp.segdata.uspto.gov/sequence.html?docid:2004034888. The polynucleotide
 CC of the invention are also useful in physical arrays of molecules and as
 CC plant breeding markers. The recombinant DNA construct is useful for
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, for conferring
 CC increased resistance to plant disease, for producing galactomannan,
 CC lignin or plant growth regulators, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This is the amino acid sequence of a plant full length insert
 CC polypeptide that can be used in the recombinant DNA construct of the
 CC invention.
 CC
 CC Sequence 229 AA;
 XX
 SQ
 Query Match 88.2%; Score 880.5; DB 8; Length 229;
 Best Local Similarity 84.5%; Pred. No. 7e-93;
 Matches 163; Conservative 19; Mismatches 10; Indels 1; Gaps 1;
 QY 1 MFLVDMFYGFGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGQHOPQYPTSEELS 60
 DB 37 MFLVDMFYGVASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEBLVQHOPQYPTSEELS 96
 QY 61 INRVKFAFDLGGHTTARWRDYAKVDAIVLVDAVDRERFAESKEKELSDLSLSDLS 120
 DB 97 IGRIRKFAFDLGGHQAIRRWKDYAKVDAVVLDVAVDERFAESKEKELDALLADSLA 156
 QY 121 QVPLVVGNGKIDIPYASSEDELRTGLT-MTGGKGVNIGDSNIRPIEFVMSIVRKMG 179
 DB 157 NVFPLIGNKIDIPYASSEELRYLGLSNFTGKGNVLADSNVRLPIFMSVVRKMG 216
 QY 180 YGEGFKMMTOYIK 192
 DB 217 YGEGFKMMSQYIK 229
 RESULT 5
 ADY05691
 ID ADY05691 standard; protein; 236 AA.
 XX

AC ADY05691;
 XX 21-APR-2005 (first entry)
 XX
 DE Plant full length insert polypeptide seqid 61506.
 XX
 KM plant protectant; plant growth regulant; gene therapy; plant;
 KM recombinant DNA construct; physical array; plant breeding marker;
 KM cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 KM extreme osmotic condition; pathogen tolerance; pest tolerance;
 KM growth rate; cell cycle pathway; disease resistance;
 KM galactomannan production; lignin production; plant growth regulator;
 KM yield; plant growth; plant development; seed oil; protein yield;
 KM protein content.
 XX
 OS Unidentified.
 XX
 FN US2004034888-A1.
 XX
 PD 19-FEB-2004.
 XX
 PF 28-APR-2003; 2003US-00425114.
 XX
 PR 06-MAY-1999; 99US-00304517.
 PR 05-NOV-2001; 2001US-00985678.
 XX
 PA (LIU/J) LIU J.
 PA (ZHOU/J) ZHOU Y.
 PA (KOVA/) KOVALIC D K.
 PA (SCRE/) SCREEN S E.
 PA (TABA/) TABASKA J E.
 PA (CAOY/) CAO Y.
 XX
 PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
 XX WPI; 2004-180133/17.
 XX
 PT New recombinant DNA construct, useful for improving plant tolerance to
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 PT pests, for conferring increased resistance to plant disease, or for
 PT improving yield.
 XX
 PS Claim 1; SEQ ID NO 61506; 15pp; English.
 XX
 PS The invention describes a recombinant DNA construct comprising a
 CC polynucleotide consisting of a sequence encoding an amino acid sequence
 CC available in electronic form from the US patent office at
 CC ftp.segdata.uspto.gov/sequence.html?docid:2004034888. The polynucleotide
 CC of the invention are also useful in physical arrays of molecules and as
 CC plant breeding markers. The recombinant DNA construct is useful for
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, for conferring
 CC increased resistance to plant disease, for producing galactomannan,
 CC lignin or plant growth regulators, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This is the amino acid sequence of a plant full length insert
 CC polypeptide that can be used in the recombinant DNA construct of the
 CC invention.
 CC
 XX Sequence 236 AA;
 SQ
 QY Query Match 88.2%; Score 880.5; DB 8; Length 236;
 DB Best Local Similarity 84.5%; Pred. No. 7.3e-93;
 Matches 163; Conservative 19; Mismatches 10; Indels 1; Gaps 1;
 1 MFVDMFYGVLASIGLWQKAKITLFLGDNAGKTTLLHMLKDEKUGOHPTQVPTSESL 60
 44 MFVDMFYGVLASIGLWQKAKITLFLGDNAGKTTLLHMLKDEKLVCHQPTQVPTSESL 103

QY 61 INRVKFAFDLGSHITARRVWRDYAKVDAIVYLVDAVDRERFAESKKEIDSLSDSLS 120
 DB 104 IGRIFKFAFDLGSHQIARRVWRDYAKVDAIVYLVDAVDRERFAESKKEIDSLSDSLS 163
 QY 121 QVPEVLGNKIDIPVASSSEDELRFTLGLT-MTNGKGTNUGDSNIRPIEFMCSIRXMG 179
 DB 164 NVFFLLIGNKIDIPVASSSEDELRFTLGLTNGKGTNUGDSNIRPIEFMCSIRXMG 223
 QY 180 YGSGFKMPTQYIK 192
 DB 224 YGSGFKMPTQYIK 236
 RESULT 6
 ID ADY08914
 ADY08914 standard; protein; 255 AA.
 XX
 AC ADY08914;
 XX
 DT 21-APR-2005 (first entry)
 XX
 DE Plant full length insert polypeptide seqid 64729.
 XX
 KM plant protectant; plant growth regulant; gene therapy; plant;
 KM recombinant DNA construct; physical array; plant breeding marker;
 KM cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 KM extreme osmotic condition; pathogen tolerance; pest tolerance;
 KM growth rate; cell cycle pathway; disease resistance;
 KM galactomannan production; lignin production; plant growth regulator;
 KM yield; plant growth; plant development; seed oil; protein yield;
 KM protein content.
 XX
 OS Unidentified.
 XX
 FN US2004034888-A1.
 XX
 PD 19-FEB-2004.
 XX
 PF 28-APR-2003; 2003US-00425114.
 XX
 PR 06-MAY-1999; 99US-00304517.
 PR 05-NOV-2001; 2001US-00985678.
 XX
 PA (LIU/J) LIU J.
 PA (ZHOU/J) ZHOU Y.
 PA (KOVA/) KOVALIC D K.
 PA (SCRE/) SCREEN S E.
 PA (TABA/) TABASKA J E.
 PA (CAOY/) CAO Y.
 XX
 PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
 XX WPI; 2004-180133/17.
 XX
 PT New recombinant DNA construct, useful for improving plant tolerance to
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 PT pests, for conferring increased resistance to plant disease, or for
 PT improving yield.
 XX
 PS Claim 1; SEQ ID NO 64729; 15pp; English.
 XX
 PS The invention describes a recombinant DNA construct comprising a
 CC polynucleotide consisting of a sequence encoding an amino acid sequence
 CC available in electronic form from the US patent office at
 CC ftp.segdata.uspto.gov/sequence.html?docid:2004034888. The polynucleotide
 CC of the invention are also useful in physical arrays of molecules and as
 CC plant breeding markers. The recombinant DNA construct is useful for
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, for conferring
 CC increased resistance to plant disease, for producing galactomannan,
 CC lignin or plant growth regulators, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of

CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This is the amino acid sequence of a plant full length insert
 CC polypeptide that can be used in the recombinant DNA construct of the
 CC invention.

XX Sequence 255 AA;

Query Match 86.9%; Score 867.5; DB 8; Length 255;
 Best Local Similarity 83.4%; Pred. No. 2.6e-91;
 Matches 161; Conservative 19; Mismatches 12; Indels 1; Gaps 1;

QY 1 MFLVDMFYGFVGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGCHOPTQPTSEELS 60
 DB 63 MFLVDMFYGFVGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLVCHOPTQPTSEELS 122
 QY 61 INRVKFAFDLGGHTTARRVWRDYAKVDAIVLVDAVDREKFAESKKEIDSLSDSL 120
 DB 123 IGRHKFAFDLGGHQTARRVWRDYAKVDAIVLVDAVDREKFAESKKEIDSLSDSL 182
 QY 121 QVPVLVGNKIDIPYASSEDELFTLGLT-MTTGKGTNVLGDSNIRPIEVFMCIVRKMG 179
 DB 183 NVFPLTIGNKKIDIPYASSEELRYHGLSNFTTGKGVNLADSNVRPLEIFMCSIVRKMG 242
 QY 180 YGEGFKMTQYIK 192
 DB 243 YGEGFKMTQYIK 255

RESULT 7

ABM74047
 ID ABM74047 standard; protein; 193 AA.

XX AC ABM74047;

DT 17-OCT-2003 (first entry)

XX DNA clone originating in barley containing SNP sequence #457.

XX Barley; single nucleotide polymorphism; SNP; genotype-phenotype analysis.

XX OS Hordeum vulgare.

XX PN W02003057877-A1.

XX PD 17-JUL-2003.

XX PF 16-DEC-2002; 2002MO-IB005403.

XX PR 20-DEC-2001; 2001JP-00387059.

XX PR 20-DEC-2001; 2001JP-00387131.

XX PR 20-DEC-2001; 2001JP-00403299.

XX PR 20-DEC-2001; 2001JP-00403300.

XX PR 27-SEP-2002; 2002JP-00327515.

XX PA (UTNT-) UNIV JAPAN OKAYAMA.

XX PI Sato K, Takeda K, Kohara Y;

XX DR WPI; 2003-587127/55.

XX PT Single nucleotide polymorphism sites in barley varieties and DNA

XX PT sequences containing them for analysis and identification of barley

XX PT varieties and production of barley transformants with desired

XX PT characteristics.

XX PS Disclosure; SEQ ID XX; 284dp; Japanese.

XX CC The present invention relates to oligonucleotide clones originating in

CC CC barley (Hordeum vulgare) which contain single nucleotide polymorphisms

CC CC (SNP). The oligonucleotides may be used for analysis of SNPs among barley

CC analysis, isolation of specific genes and creation of new varieties by
 CC transformation of barley varieties with them and production of new barley
 CC varieties with desired properties. The present sequence represents an
 CC oligonucleotide clone sequence featured in the specification. The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published-pct-sequences

XX Sequence 193 AA;

Query Match 86.8%; Score 866.5; DB 7; Length 193;
 Best Local Similarity 83.9%; Pred. No. 2.3e-91;
 Matches 162; Conservative 19; Mismatches 11; Indels 1; Gaps 1;

QY 1 MFLVDMFYGFVGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGCHOPTQPTSEELS 60
 DB 1 MFLVDMFYGFVGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLVCHOPTQPTSEELS 60
 QY 61 INRVKFAFDLGGHTTARRVWRDYAKVDAIVLVDAVDREKFAESKKEIDSLSDSL 120
 DB 61 IGRHKFAFDLGGHQTARRVWRDYAKVDAIVLVDAVDREKFAESKKEIDSLSDSL 120
 QY 121 QVPVLVGNKIDIPYASSEDELFTLGLT-MTTGKGTNVLGDSNIRPIEVFMCIVRKMG 179
 DB 121 TVFPLTIGNKKIDIPYASSEELRYHGLSNFTTGKGVNLADSNVRPLEIFMCSIVRKMG 180
 QY 180 YGEGFKMTQYIK 192
 DB 181 YGEGFKMTQYIK 193

RESULT 8

AAG30108
 ID AAG30108 standard; protein; 193 AA.

XX AC AAG30108;

DT 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 35936.

XX Protein identification; signal transduction pathway; metabolic pathway;

XX KM hybridisation assay; genetic mapping; gene expression control; promoter;

XX KM termination sequence.

XX OS Arabidopsis thaliana.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-00301439.

XX PR 25-FEB-1999; 99US-0121825P.

XX PR 05-MAR-1999; 99US-0123180P.

XX PR 09-MAR-1999; 99US-0123548P.

XX PR 23-MAR-1999; 99US-0125788P.

XX PR 29-MAR-1999; 99US-0126264P.

XX PR 01-APR-1999; 99US-0126785P.

XX PR 06-APR-1999; 99US-0128234P.

XX PR 08-APR-1999; 99US-0128714P.

XX PR 16-APR-1999; 99US-0129845P.

XX PR 21-APR-1999; 99US-0130077P.

XX PR 23-APR-1999; 99US-0130510P.

XX PR 23-APR-1999; 99US-0130891P.

XX PR 28-APR-1999; 99US-0131449P.

XX PR 30-APR-1999; 99US-0132048P.

XX PR 04-MAY-1999; 99US-0132407P.

XX PR 05-MAY-1999; 99US-0132484P.

XX PR 06-MAY-1999; 99US-0132485P.

XX PR 06-MAY-1999; 99US-0132486P.

PR 06-MAY-1999; 99US-0122487P.
PR 07-MAY-1999; 99US-0122863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.

PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 25-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 08-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149930P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 25-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152263P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 26-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156569P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159658P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.

PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 86.4%; Score 862.5; DB 3; Length 193;

Best Local Similarity 82.9%; Pred. No. 6.6e-91; Mismatches 11; Indels 1; Gaps 1;

Matches 160; Conservative 21; Mismatches 11; Indels 1; Gaps 1;

QY 1 MFLVDMFYGFLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGQHOPOTYPTSEELS 60
DB 1 MFLVDMFYGFLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGQHOPOTYPTSEELS 60
QY 61 INRVKFKAPDLGSHHTTARVWRDYAKVDAIVLVDAVDRERPAESKKEIDSLSDSLS 120
DB 61 IGRKIKFKAPDLGSHHTTARVWRDYAKVDAIVLVDAVDRERPAESKKEIDSLSDSLSLA 120
QY 121 QVPVLVGNKIDIPYASSEDELRFTGLT-MTTGKGTVNIGDSNIRPIEVFMCSIVRKMG 179
DB 121 SVFPLILGNKIDIPYASSEDELRFTGLT-MTTGKGTVNIGDSNIRPIEVFMCSIVRKMG 180
QY 180 YGSGFKMTQYIK 192
DB 181 YGSGFKMTQYIK 193

RESULT 9

ABG59985 ID ABG59985 standard; protein; 208 AA.

XX ABG59985;

DT 30-JUL-2002 (first entry)

DE Human DITHP polypeptide #43.

XX Human, DITHP, diagnostic and therapeutic polypeptide; bone; testis; skin;
KM cell proliferative disorder; cancer; tumour; autoimmune disorder; brain;
KM inflammatory disorder; viral infection; bacterial infection; seizure;
KM fungal infection; parasitic infections; developmental disorder; breast;
KM endocrine disorder; metabolic disorder; neurological disorder; cervix;
KM gastrointestinal disorder; transport disorder; gene therapy; kidney;
KM adrenal gland; bone marrow; lung; ovary; pancreas; prostate; spleen;
KM thymus.

XX Homo sapiens.

XX WO200220754-A2.

PD 14-MAR-2002.

PF 29-AUG-2001, 2001WO-US027127.

XX 05-SEP-2000; 2000US-0229747P.
PR 05-SEP-2000; 2000US-0229748P.
PR 05-SEP-2000; 2000US-0229749P.
PR 05-SEP-2000; 2000US-0229750P.
PR 05-SEP-2000; 2000US-0229751P.
PR 05-SEP-2000; 2000US-0230583P.
PR 06-SEP-2000; 2000US-0230514P.
PR 06-SEP-2000; 2000US-0230515P.
PR 06-SEP-2000; 2000US-0230517P.

PR 06-SEP-2000; 2000US-0230518P.
PR 06-SEP-2000; 2000US-0230519P.
PR 06-SEP-2000; 2000US-0230559P.
PR 06-SEP-2000; 2000US-0230597P.
PR 06-SEP-2000; 2000US-0230598P.
PR 06-SEP-2000; 2000US-0230599P.
PR 06-SEP-2000; 2000US-0230610P.
PR 06-SEP-2000; 2000US-0230655P.
PR 06-SEP-2000; 2000US-0230988P.
PR 07-SEP-2000; 2000US-0230951P.
PR 07-SEP-2000; 2000US-0231163P.
PR 07-SEP-2000; 2000US-0231167P.

XX (INCYTE GENOMICS INC.

XX Stuart J, Lincoln SE, Altus CM, Dufour GE, Chalup MS, Hillman JL;
PI Jones AM, Yu JY, Wright R, Gietzen D, Liu TF, Yap PE, Dahl CR;
PI Momiyama MG, Bradley DU, Rohatgi SD, Harris B, Roseberry AM;
PI Gerstin EH, Peralta CH, David MH, Panzer SR, Flores V, Daffo A;
PI Marwaha R, Chen AJ, Chang SC, Au AP, Imman RR;
DR WPI, 2002-383054/41.
DR N-PSDB; ABR71577.

An isolated polynucleotide useful in diagnostics and therapeutics.

PS Claim 29; Page 557; 686pp; English.

XX The invention relates to human diagnostic and therapeutic (dithp)
CC polynucleotides and their associated polypeptides (DITHP polypeptides).
CC The sequences of the invention are used in the treatment and diagnosis of
CC cell proliferative disorders (e.g. atherosclerosis, cirrhosis), cancers
CC (e.g. tumours of the adrenal gland, bone, bone marrow, brain, breast,
CC cervix, kidney, lung, ovary, pancreas, prostate, skin, spleen, testis or
CC thymus), autoimmune/inflammatory disorders (e.g. asthma, bronchitis,
CC psoriasis, osteoporosis), viral infections, bacterial infections, fungal
CC infections, parasitic infections, developmental disorders (e.g. anaemia,
CC epilepsy), seizure disorders (e.g. cerebral palsy, spina bifida),
CC endocrine disorders (e.g. thrombosis, aneurysm), metabolic disorders
CC (e.g. obesity, diabetes), neurological disorders (e.g. stroke,
CC amyotrophic lateral sclerosis, multiple sclerosis), gastrointestinal
CC disorders (e.g. ulcerative colitis, lysinuria) and transport disorders
CC (e.g. myotonic dystrophy, catatonias, peripheral neuropathy). Sequences
CC ABG59943-ABG60220 represent human DITHP polypeptides of the invention
XX

SQ Sequence 208 AA;

Query Match 86.4%; Score 862.5; DB 5; Length 208;

Best Local Similarity 82.9%; Pred. No. 7.4e-91; Mismatches 11; Indels 1; Gaps 1;

Matches 160; Conservative 21; Mismatches 11; Indels 1; Gaps 1;

QY 1 MFLVDMFYGFLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGQHOPOTYPTSEELS 60
DB 16 MFLVDMFYGFLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGQHOPOTYPTSEELS 75
QY 61 INRVKFKAPDLGSHHTTARVWRDYAKVDAIVLVDAVDRERPAESKKEIDSLSDSLS 120
DB 76 IGRKIKFKAPDLGSHHTTARVWRDYAKVDAIVLVDAVDRERPAESKKEIDSLSDSLSLA 135
QY 121 QVPVLVGNKIDIPYASSEDELRFTGLT-MTTGKGTVNIGDSNIRPIEVFMCSIVRKMG 179
DB 136 NVFPLILGNKIDIPYASSEDELRFTGLT-MTTGKGTVNIGDSNIRPIEVFMCSIVRKMG 195
QY 180 YGSGFKMTQYIK 192
DB 196 YGSGFKMTQYIK 208

RESULT 10

ADX88378 ID ADX88378 standard; protein; 208 AA.

XX ADX88378;

XX 21-APR-2005 (first entry)
DT Plant full length insert polypeptide seqid 51042.
XX
XX plant protectant; plant growth regulator; gene therapy; plant;
KM recombinant DNA construct; physical array; plant breeding marker;
KM cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KM extreme osmotic condition; pathogen tolerance; pest tolerance;
KM growth rate; cell cycle pathway; disease resistance;
KM galactomannan production; lignin production; plant growth regulator;
KM yield; plant growth; plant development; seed oil; protein yield;
KM protein content.
KM
XX
XX
XX
XX US2004034888-A1.
XX
XX 19-FEB-2004.
XX
XX 28-APR-2003; 2003US-00425114.
XX
XX 06-MAY-1999; 99US-00304517.
XX PR 05-NOV-2001; 2001US-00985678.
XX
XX (LIU/) LIU J.
XX PA (ZHOU/) ZHOU Y.
XX PA (KOVA/) KOVALIC D K.
XX PA (SCRE/) SCREEN S E.
XX PA (TABAS/) TABASKA J E.
XX PA (CAO/) CAO Y.
XX
XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX WPI; 2004-180133/17.
XX
XX New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
XX
XX Claim 1; SEQ ID NO 51042; 15pp; English.
XX
XX The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This is the amino acid sequence of a plant full length insert
CC polypeptide that can be used in the recombinant DNA construct of the
CC invention.
XX
XX Sequence 208 AA;
XX
XX
XX
XX Query Match 86.4%; Score 862.5; DB 8; Length 208;
XX Best Local Similarity 82.9%; Pred. No. 7.4e-91;
XX Matches 160; Conservative 21; Mismatches 11; Indels 1; Gaps 1;
Oy 1 MFLVDMFGFLASIGLMOKKAKILFLGDMNGKTTLLMLKDEKLGQHPTPTSESL 60
Db 16 MFLVDMFGFLASIGLMOKKAKILFLGDMNGKTTLLMLKDEKLGQHPTPTSESL 75
Oy 61 INRVKFAFDLGGHTIARRVNRDYYAKVAIVLVDAVDRERFASKEKELSDLS 120

Db 76 IGRKFKAPDLGGHQIARRWKDYAKVDAVVLVAYVDERFASKEKELSDLS 135
Oy 121 QVFLVLTGNKIDIPYASSEDELRFTGLT-MTGGKGVNIGDSNIPPIEFMGSIVRK 179
Db 136 NVFFLLGNKIDIPYASSEELRHYHGLSNFTTGKGVNIGDSNVPLIEFMGSIVRK 195
Oy 180 YGEGFPMWTOYIK 192
Db 196 YGDGFKWVSQYIK 208
RESULT 11
ADY07438
ID ADY07438 standard; protein; 236 AA.
XX
XX
XX AC ADY07438;
XX
XX
XX DT 21-APR-2005 (first entry)
XX
XX DE Plant full length insert polypeptide seqid 63253.
XX
XX KM plant protectant; plant growth regulator; gene therapy; plant;
KM recombinant DNA construct; physical array; plant breeding marker;
KM cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KM extreme osmotic condition; pathogen tolerance; pest tolerance;
KM growth rate; cell cycle pathway; disease resistance;
KM galactomannan production; lignin production; plant growth regulator;
KM yield; plant growth; plant development; seed oil; protein yield;
KM protein content.
KM
XX
XX
XX
XX
XX
XX
XX
XX
XX US2004034888-A1.
XX
XX
XX 19-FEB-2004.
XX
XX 28-APR-2003; 2003US-00425114.
XX
XX 06-MAY-1999; 99US-00304517.
XX PR 05-NOV-2001; 2001US-00985678.
XX
XX (LIU/) LIU J.
XX PA (ZHOU/) ZHOU Y.
XX PA (KOVA/) KOVALIC D K.
XX PA (SCRE/) SCREEN S E.
XX PA (TABAS/) TABASKA J E.
XX PA (CAO/) CAO Y.
XX
XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX WPI; 2004-180133/17.
XX
XX New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
XX
XX Claim 1; SEQ ID NO 63253; 15pp; English.
XX
XX The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake

CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This is the amino acid sequence of a plant full length insert
CC polypeptide that can be used in the recombinant DNA construct of the
CC invention.

XX Sequence 236 AA;

Query Match 86.4%; Score 862.5; DB 8; Length 236;
Best Local Similarity 82.9%; Pred. No. 8.9e-91;
Matches 160; Conservative 21; Mismatches 11; Indels 1; Gaps 1;

QY 1 MFLVDFVYGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGCHOPTQYPTSEELS 60
DB MFLMDVYVGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKRLVQHPTQPTSEELS 103
QY 61 INRVKFAFDLGGHTTARRVWRDYAKVDAIVYLVDVREPERAESKKEIDSLSDSLA 120
DB 104 IGIKFKFAPDLGGHQAIRRWKDYAKVDAIVYLVDVREPERAESKKEIDSLSDSLA 163
QY 121 QVPLVILGNKIDIPYASSEDELRTLTGLT-MTTGKGVNMGDSNIRPIEFVFMCSIVRKMG 179
DB 164 NVFPLILGNKIDIPYASSEELRYHLGLSNFTTGKGVNLGDSNVRLPEVFMCSIVRKMG 223
QY 180 YGGEFKMTQYIK 192
DB 224 YGDGFKMVQYIK 236

RESULT 12
ADY07420
ID ADY07420 standard; protein; 244 AA.

AC ADY07420;
DT 21-APR-2005 (first entry)

XX Plant full length insert polypeptide seqid 63235.

XX plant protectant; plant growth regulant; gene therapy; plant;
XX recombinant DNA construct; physical array; plant breeding marker;
XX cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
XX extreme osmotic condition; pathogen tolerance; pest tolerance;
XX growth rate; cell cycle pathway; disease resistance;
XX galactomannan production; lignin production; plant growth regulator;
XX yield; plant growth; plant development; seed oil; protein yield;
XX protein content.

XX Unidentified.

XX US2004034888-A1.

XX 19-FEB-2004.

XX 28-APR-2003; 2003US-00425114.

XX 06-MAY-1999; 99US-00304517.
XX 05-NOV-2001; 2001US-00985678.

PA (LIU/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABAS/) TABASKA J E.
PA (CAO/) CAO Y.

PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;

XX WPI; 2004-180133/17.

XX New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for

PT improving yield.

XX Claim 1; SEQ ID NO 63235; 15pp; English.

XX The invention describes a recombinant DNA construct comprising a
XX polynucleotide consisting of a sequence encoding an amino acid sequence
XX available in electronic form from the US patent office at
XX ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
XX of the invention are also useful in physical arrays of molecules and as
XX plant breeding markers. The recombinant DNA construct is useful for
XX improving plant tolerance to cold, heat, drought, herbicides, extreme
XX osmotic conditions, pathogens or pests, for manipulating growth rate in
XX plant cells by modification of the cell cycle pathway, for conferring
XX increased resistance to plant disease, for producing galactomannan,
XX lignin or plant growth regulators, for increasing the rate of homologous
XX recombination in plants, for improving yield by modification of
XX photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
XX or by providing improved plant growth and development under at least one
XX stress condition or for modifying seed oil or protein yield and/or
XX content. This is the amino acid sequence of a plant full length insert
XX polypeptide that can be used in the recombinant DNA construct of the
XX invention.

XX Sequence 244 AA;

Query Match 86.4%; Score 862.5; DB 8; Length 244;
Best Local Similarity 82.9%; Pred. No. 9.3e-91;
Matches 160; Conservative 21; Mismatches 11; Indels 1; Gaps 1;

QY 1 MFLVDFVYGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGCHOPTQYPTSEELS 60
DB 52 MFLMDVYVGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKRLVQHPTQPTSEELS 111
QY 61 INRVKFAFDLGGHTTARRVWRDYAKVDAIVYLVDVREPERAESKKEIDSLSDSLA 120
DB 112 IGIKFKFAPDLGGHQAIRRWKDYAKVDAIVYLVDVREPERAESKKEIDSLSDSLA 171
QY 121 QVPLVILGNKIDIPYASSEDELRTLTGLT-MTTGKGVNMGDSNIRPIEFVFMCSIVRKMG 179
DB 172 NVFPLILGNKIDIPYASSEELRYHLGLSNFTTGKGVNLGDSNVRLPEVFMCSIVRKMG 231
QY 180 YGGEFKMTQYIK 192
DB 232 YGDGFKMVQYIK 244

RESULT 13
ADY87922
ID ADY87922 standard; protein; 251 AA.

XX ADY87922;

XX 21-APR-2005 (first entry)

XX Plant full length insert polypeptide seqid 50586.

XX plant protectant; plant growth regulant; gene therapy; plant;
XX recombinant DNA construct; physical array; plant breeding marker;
XX cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
XX extreme osmotic condition; pathogen tolerance; pest tolerance;
XX growth rate; cell cycle pathway; disease resistance;
XX galactomannan production; lignin production; plant growth regulator;
XX yield; plant growth; plant development; seed oil; protein yield;
XX protein content.

XX Unidentified.

XX US2004034888-A1.

XX 19-FEB-2004.

XX 28-APR-2003; 2003US-00425114.

PR 06-MAY-1999; 99US-00304517.
PR 05-NOV-2001; 2001US-00985678.
XX
XX (LIU/J.) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABAS/) TABASKA J E.
PA (CAOY/) CAO Y.
XX
XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX WPI; 2004-180133/17.
XX
XX New recombinant DNA construct, useful for improving plant tolerance to
XX cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
XX pests, for conferring increased resistance to plant disease, or for
XX improving yield.
XX
XX Claim 1; SEQ ID NO 50586; 15pp; English.
XX
XX The invention describes a recombinant DNA construct comprising a
XX polynucleotide consisting of a sequence encoding an amino acid sequence
XX available in electronic form from the US patent office at
XX ftp.segdata.uspto.gov/sequence.html?docid:2004034888. The polynucleotide
XX of the invention are also useful in physical arrays of molecules and as
XX plant breeding markers. The recombinant DNA construct is useful for
XX improving plant tolerance to cold, heat, drought, herbicides, extreme
XX osmotic conditions, pathogens or pests, for manipulating growth rate in
XX plant cells by modification of the cell cycle pathway, for conferring
XX increased resistance to plant disease, for producing galactomannan,
XX lignin or plant growth regulators, for increasing the rate of homologous
XX recombination in plants, for improving yield by modification of
XX photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
XX or by providing improved plant growth and development under at least one
XX stress condition or for modifying seed oil or protein yield and/or
XX content. This is the amino acid sequence of a plant full length insert
XX polypeptide that can be used in the recombinant DNA construct of the
XX invention.
XX
XX Sequence 251 AA;
SQ
Query Match 86.4%; Score 862.5; DB 8; Length 251;
Best Local Similarity 82.9%; Pred. No. 9.7e-91;
Matches 160; Conservative 21; Mismatches 11; Indels 1; Gaps 1;
QY 1 MFLVDMFYGPIASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGQHPTQYPTSEELS 60
DB 59 MFLMDMFYGVLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDERLVQHPTQPTSEELS 118
QY 61 INRVKFAFDLGGHTIARRVWDYAKVDAIVYLVDADVDERFAESKKELDLSDLSLS 120
DB 119 IGTKIKFAFDLGGHGIARRVWKDYAKVDAIVYLVDADVDERFAESKKELDLSDLSLA 178
QY 121 QVPVLVGNKIDIPYASSEBELRFTLGLT-MTTGKGTVNLGDSNIRPIEVNCSIVKXMG 179
DB 179 NVPFILILGNKIDIPYASSEBELRYHLGLSNFTTGKGNLSDSNVRPLEVFCSVVRKMG 238
QY 180 YGEGFKMTTOYIK 192
DB 239 YGDGFKMVSQYIK 251
XX
XX RESULT 14
XX ADY10442
XX ID ADY10442 standard; protein; 280 AA.
XX
XX ADY10442;
XX
XX 21-APR-2005 (first entry)
XX
XX Plant full length insert polypeptide seqid 66257.
XX

KW plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content.
XX
XX Unidentified.
XX
XX US2004034888-A1.
XX
XX
XX 19-FEB-2004.
XX
XX 28-APR-2003; 2003US-00425114.
XX
XX 06-MAY-1999; 99US-00304517.
XX 05-NOV-2001; 2001US-00985678.
XX
XX (LIU/J.) LIU J.
XX (ZHOU/) ZHOU Y.
XX (KOVA/) KOVALIC D K.
XX (SCRE/) SCREEN S E.
XX (TABAS/) TABASKA J E.
XX (CAOY/) CAO Y.
XX
XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX WPI; 2004-180133/17.
XX
XX New recombinant DNA construct, useful for improving plant tolerance to
XX cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
XX pests, for conferring increased resistance to plant disease, or for
XX improving yield.
XX
XX Claim 1; SEQ ID NO 66257; 15pp; English.
XX
XX The invention describes a recombinant DNA construct comprising a
XX polynucleotide consisting of a sequence encoding an amino acid sequence
XX available in electronic form from the US patent office at
XX ftp.segdata.uspto.gov/sequence.html?docid:2004034888. The polynucleotide
XX of the invention are also useful in physical arrays of molecules and as
XX plant breeding markers. The recombinant DNA construct is useful for
XX improving plant tolerance to cold, heat, drought, herbicides, extreme
XX osmotic conditions, pathogens or pests, for manipulating growth rate in
XX plant cells by modification of the cell cycle pathway, for conferring
XX increased resistance to plant disease, for producing galactomannan,
XX lignin or plant growth regulators, for increasing the rate of homologous
XX recombination in plants, for improving yield by modification of
XX photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
XX or by providing improved plant growth and development under at least one
XX stress condition or for modifying seed oil or protein yield and/or
XX content. This is the amino acid sequence of a plant full length insert
XX polypeptide that can be used in the recombinant DNA construct of the
XX invention.
XX
XX Sequence 280 AA;
SQ
Query Match 86.4%; Score 862.5; DB 8; Length 280;
Best Local Similarity 82.9%; Pred. No. 1.1e-90;
Matches 160; Conservative 21; Mismatches 11; Indels 1; Gaps 1;
QY 1 MFLVDMFYGPIASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGQHPTQYPTSEELS 60
DB 88 MFLMDMFYGVLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDERLVQHPTQPTSEELS 147
QY 61 INRVKFAFDLGGHTIARRVWDYAKVDAIVYLVDADVDERFAESKKELDLSDLSLS 120
DB 148 IGTKIKFAFDLGGHGIARRVWKDYAKVDAIVYLVDADVDERFAESKKELDLSDLSLA 207
QY 121 QVPVLVGNKIDIPYASSEBELRFTLGLT-MTTGKGTVNLGDSNIRPIEVNCSIVKXMG 179
XX

DB 208 NVEFLILGNKIDIPYAASEELRYHLGLSNFTTGKGNLSDSNVPLEVFMCSIVRKMG 267
QY 180 YGEGFKMTQYIK 192
||:||||:||||
DB 268 YGDGFKMVSQYIK 280

RESULT 15
AD75842
ID ADX75842 standard; protein; 266 AA.
XX
AC ADX75842;
XX
DT 21-APR-2005 (first entry)
XX
DE Plant full length insert polypeptide seqid 45208.
XX
KM plant protectant; plant growth regulator; gene therapy; plant;
KM recombinant DNA construct; physical array; plant breeding marker;
KM cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KM extreme osmotic condition; pathogen tolerance; pest tolerance;
KM growth rate; cell cycle pathway; disease resistance;
KM galactomannan production; lignin production; plant growth regulator;
KM yield; plant growth; plant development; seed oil; protein yield;
KM protein content.
XX
OS Unidentified.
XX
PN US2004034888-A1.
XX
PD 19-FEB-2004.
XX
PE 28-APR-2003; 2003US-00425114.
XX
PR 06-MAY-1999; 99US-00304517.
PR 05-NOV-2001; 2001US-00985678.
XX
PA (LIU/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABAS/) TABASKA J E.
PA (CAOY/) CAO Y.
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX
XX WPI; 2004-180133/17.
XX
PT New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
PS
PS Claim 1; SEQ ID NO 45208; 15pp; English.
XX
XX The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.segdata.uspo.gov/sequence.html?DocID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This is the amino acid sequence of a plant full length insert
CC polypeptide that can be used in the recombinant DNA construct of the
CC invention.

XX
SQ Sequence 266 AA;
Query Match 86.1%; Score 859.5; DB 8; Length 266;
Best Local Similarity 82.9%; Pred. No. 2.4e-90;
Matches 160; Conservative 19; Mismatches 13; Indels 1; Gaps 1;
QY 1 MFLVDMFYGLASIGIMQKAKILFLGLDNAGKTTLLHMLKDEKLGQHPTQYPTSEELS 60
DB 74 MFLFDWFGILASLIGIMQKAKILFLGLDNAGKTTLLHMLKDEKRLVQHPTQYPTSEELS 133
QY 61 INRVKFKAPDLCGHTIARRVWRDYAKVDATYYLVDAVDREKFAASKKELDLSLSDSLS 120
DB 134 IGRIFKAPDLGQHQIARRVWMDYYAKVDAAVYLVDAVDKERFAASKKELDLSLSDSLSLT 193
QY 121 QYPUVLGNKIDIPYAASEELRYHLGLTNFTTGKGNVLDSDSNVPLEVFMCSIVRKMG 179
DB 194 TVPFLILGNKIDIPYAASEELRYHLGLTNFTTGKGNVLDSDSNVPLEVFMCSIVRKMG 253
QY 180 YGEGFKMTQYIK 192
DB 254 YGDGFKMVSQYIK 266

Search completed: December 9, 2005, 01:35:04
Job time : 137 secs

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OM protein - protein search, using sw model

Run on: December 9, 2005, 01:13:16 ; Search time 38 Seconds
(without alignments)
486.148 Million cell updates/sec

Title: US-10-688-481-11

Perfect score: 998
Sequence: 1 MFLVDMFYGLASIGLMQKE.....SIVRKMGYGEGRKMTQYIK 192

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	871.5	87.3	193	2	T52096 small GTP-binding
2	863.5	86.5	193	2	S42528 GTP-binding protei
3	862.5	86.4	193	2	T01509 GTP-binding protei
4	854.5	85.6	193	2	T16964 GTP-binding protei
5	850.5	85.2	193	2	S28603 GTP-binding protei
6	848.5	85.0	193	2	T52094 small GTP-binding
7	843.5	84.5	193	2	T52095 ras-like small mon
8	835.5	83.7	193	2	T16993 GTP-binding protei
9	832	83.4	194	2	T16969 GTP-binding protei
10	822.5	82.4	193	2	D86224 hypothetical prote
11	706	70.7	198	2	T03696 GTP-binding protei
12	628.5	63.0	190	2	S28605 GTP-binding protei
13	625	62.6	190	2	S71588 GTP-binding protei
14	593.5	59.5	193	2	T29706 GTP-binding protei
15	585.5	58.7	198	2	S39543 GTP-binding protei
16	562	56.3	190	2	A33619 GTP-binding protei
17	521	52.2	111	2	S71589 GTP-binding protei
18	297.5	29.8	190	2	T09136 ADP-riboylation f
19	277.5	27.8	184	2	T21126 ADP-riboylation f
20	275	27.6	181	2	A54022 ADP-riboylation f
21	274	27.5	182	2	T22655 ADP-riboylation f
22	271.5	27.2	182	2	B54869 ADP-riboylation f
23	271.5	27.2	183	2	S46035 ADP-riboylation f
24	270	27.1	180	2	A40438 GTP-binding protei
25	269.5	27.0	182	2	A54869 ADP-riboylation f
26	267.5	26.8	182	2	S41938 ADP-riboylation f
27	261	26.2	175	2	T31519 ADP-riboylation f
28	259.5	26.0	175	4	I50632 hypothetical CP81
29	257.5	25.8	175	2	B23741 ADP-riboylation f

30	257.5	25.8	175	2	JC4950 ADP-riboylation f
31	253	25.4	183	2	D49993 ADP-riboylation f
32	250.5	25.1	180	2	T32978 ADP-riboylation f
33	250.5	25.1	191	2	S29608 ADP-riboylation f
34	250	25.1	182	2	C49893 ADP-riboylation f
35	249.5	25.0	175	2	B53859 ADP-riboylation f
36	248.5	24.9	179	2	JH0260 ADP-riboylation f
37	243.5	24.4	178	2	S40940 ADP-riboylation f
38	243.5	24.4	181	2	A36367 ADP-riboylation f
39	242.5	24.3	180	1	S37599 ADP-riboylation f
40	242.5	24.3	181	2	B36167 ADP-riboylation f
41	241.5	24.2	181	2	T52341 ADP-riboylation f
42	241	24.1	182	2	A49520 ADP-riboylation f
43	240.5	24.1	181	2	A41570 ADP-riboylation f
44	240.5	24.1	181	2	T52339 ADP-riboylation f
45	240.5	24.1	181	2	S49325 ADP-riboylation f

ALIGNMENTS

```
RESULT 1
T52096
small GTP-binding protein Sar1Bnt [imported] - common tobacco
C:Species: Nicotiana tabacum (common tobacco)
C:Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
C:Accession: T52096
R:Andreeva, A.V.; Kutuzov, M.A.; Evans, D.E.; Hawes, C.R.
submitted to the EMBL data library, December 1999
A:Description: Plant proteins involved in membrane transport between the endoplasmic reti
A:Reference number: Z25950
A:Accession: T52096
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-193 <AND>
A:Cross-references: UNIPROT:Q9SD05; UNIPARC:UP100000ACFAF; EMBL:AF210431; PDB:AAF17254.1
C:Superfamily: ADP-riboylation factor

Query Match      87.3%; Score 871.5; DB 2; Length 193;
Best Local Similarity 83.4%; Pred. No. 4.9e-69;
Matches 161; Conservative 21; Mismatches 10; Indels 1; Gaps 1;

QY 1 MFLVDMFYGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGCHQPTQYPTSELS 60
DB 1 MFLVDMFYGLATLGLMQEAKILFLGLDNAGKTTLLHMLKDEKLVQHQPPTSELS 60
QY 61 INRVKRAPDLGGHTIARRVWRDYAKVDAIVYLVDVDEREFAESKKELDLSDDSL 120
DB 61 IGRKFAFDLGGHQLARRVWKDYAKVDAIVYLVDSPDERFAESKKELDALLSDSLA 120
QY 121 QVVLVLGNKIDIPYASSEDELFPTIGLT-MTGGKTVNLGDSNIRPIEFMCSIVRKM 179
DB 121 TVFLLIGNKIDIPYASSEDELFHMLGTGVTGKRVNLADSNVRVEVFMCSIVRKM 180
QY 180 YGEGFKMTQYIK 192
DB 181 YGEGFRMSQYIK 193

RESULT 2
S42528
GTP-binding protein SAR1 homolog - tomato
N:Alternate names: GTPase-like protein
C:Species: Lycopersicon esculentum (tomato)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S42528
R:Davies, C.
Plant Mol. Biol. 24, 525-531, 1994
A:Title: Cloning and characterization of a tomato GTPase-like gene related to yeast and J
A:Reference number: S42528; MUID:94169306; PMID:8123794
A:Accession: S42528
A:Molecule type: mRNA
A:Residues: 1-193 <DAV>
```

A;Cross-references: UNIPROT:P52884; UNIPARC:UPI0000135564; EMBL:L12051; NID:q473683; PID:
C;Function:
A;Description: involved in vesicular transport
C;Superfamily: ADP-riboseylation factor
C;Keywords: GTP binding; nucleotide binding; P-loop
F;27-34/Region: nucleotide-binding motif A (P-loop)
F;129-132/Region: GTP-binding NKXD motif

Query Match 86.5%; Score 863.5; DB 2; Length 193;
Best Local Similarity 83.9%; Pred. No. 2.5e-68;
Matches 162; Conservative 16; Mismatches 14; Indels 1; Gaps 1;

QY 1 MFLVDMFYGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGQHOPQYPTSEELS 60
DB 1 MFLVDMFYGLASIGLMQKDKKILFLGLDNAGKTTLLHMLKDEKLVQHOPQYPTSEELS 60
QY 61 INRVKFAFDLGGHTTARRVWRDYAKVDALVYLVDAVDRERFESKKEIDSLSDSL 120
DB 61 IGKIKFAFDLGGHQAIRRVWRDYAKVDALVYLVDAVDRERFESKKEIDSLSDSL 120
QY 121 QVPLVLGNKIDIPYASSEDELRLFTLGLT-MTTGKGVNLGDSNIRPIEVFMCISYVRKM 179
DB 121 NVPLLIIGNKIDIPYASSEDELRLVHLGLTGVTTGKGNINLAGTVVRPIEVFMCISYVRKM 180
QY 180 YGEGFKMMSOYIK 192
DB 181 YGEGFKMMSOYIK 193

RESULT 3

T01509
GTP-binding protein T10M13.9 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 19-Feb-1999 #sequence_revision 19-1999 #text_change 09-Jul-2004
R;Johnson, A.F.; de la Bastide, M.; Lodhi, M.; Hoffman, J.; Hasegawa, A.; Gnoj, L.; Gott
Martensen, R.; McCombie, W.
Submitted to the EMBL Data Library, May 1997
A;Description: The sequence of the Arabidopsis thaliana T10M13 BAC.
A;Reference number: Z14346
A;Accession: T01509
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-193 <JCH>
A;Cross-references: UNIPROT:O04834; UNIPARC:UPI000001457; EMBL:AF001308; NID:g2104523;
A;Experimental source: cultivar Columbia
C;Genetics:
A;Map position: 4S
A;Intons: 43/3; 87/3
A;Note: T10M13.9
C;Superfamily: ADP-riboseylation factor
C;Keywords: GTP binding; nucleotide binding; P-loop
F;27-34/Region: nucleotide-binding motif A (P-loop)
F;129-132/Region: GTP-binding NKXD motif

Query Match 86.4%; Score 862.5; DB 2; Length 193;
Best Local Similarity 82.9%; Pred. No. 3e-68;
Matches 160; Conservative 21; Mismatches 11; Indels 1; Gaps 1;

QY 1 MFLVDMFYGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGQHOPQYPTSEELS 60
DB 1 MFLVDMFYGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLVQHOPQYPTSEELS 60
QY 61 INRVKFAFDLGGHTTARRVWRDYAKVDALVYLVDAVDRERFESKKEIDSLSDSL 120
DB 61 IGKIKFAFDLGGHQAIRRVWRDYAKVDALVYLVDAVDRERFESKKEIDSLSDSL 120
QY 121 QVPLVLGNKIDIPYASSEDELRLFTLGLT-MTTGKGVNLGDSNIRPIEVFMCISYVRKM 179
DB 121 NVPLLIIGNKIDIPYASSEDELRLVHLGLSFTTGKGNINLAGTVVRPIEVFMCISYVRKM 180
QY 180 YGEGFKMMSOYIK 192
DB 181 YGEGFKMMSOYIK 193

DB 181 YGEGFKMMSOYIK 193

RESULT 4

T16964
GTP-binding protein - curled-leaved tobacco
C;Species: Nicotiana glauca (curled-leaved tobacco)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
A;Accession: T16964
R;Borisejuk, N.
Submitted to the EMBL Data Library, September 1996
A;Reference number: Z16620
A;Accession: T16964
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-193 <BOR>
A;Cross-references: UNIPROT:O24110; UNIPARC:UPI00000A192; EMBL:Y08423
C;Superfamily: ADP-riboseylation factor
C;Keywords: GTP binding; nucleotide binding; P-loop
F;27-34/Region: nucleotide-binding motif A (P-loop)
F;129-132/Region: GTP-binding NKXD motif

Query Match 85.6%; Score 854.5; DB 2; Length 193;
Best Local Similarity 82.4%; Pred. No. 1.5e-67;
Matches 159; Conservative 21; Mismatches 12; Indels 1; Gaps 1;

QY 1 MFLVDMFYGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGQHOPQYPTSEELS 60
DB 1 MFLVDMFYGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLVQHOPQYPTSEELS 60
QY 61 INRVKFAFDLGGHTTARRVWRDYAKVDALVYLVDAVDRERFESKKEIDSLSDSL 120
DB 61 IGKIKFAFDLGGHQAIRRVWRDYAKVDALVYLVDAVDRERFESKKEIDSLSDSL 120
QY 121 QVPLVLGNKIDIPYASSEDELRLFTLGLT-MTTGKGVNLGDSNIRPIEVFMCISYVRKM 179
DB 121 TVPLLIIGNKIDIPYASSEDELRLVHLGLTGVTTGKGNINLAGTVVRPIEVFMCISYVRKM 180
QY 180 YGEGFKMMSOYIK 192
DB 181 YGEGFKMMSOYIK 193

RESULT 5

S28603
GTP-binding protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S28603
R;D'Entfert, C.; Genesee, M.; Galliardin, C.
EMBO J. 11, 4205-4211, 1992
A;Title: Pission yeast and a plant have functional homologues of the Sar1 and Sec12 prote
A;Reference number: S28603; NID:93011016; PMID:1396601
A;Accession: S28603
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-193 <ENF>
A;Cross-references: UNIPROT:Q01474; UNIPARC:UPI0000001400; GB:M95795; NID:g16733; PIDN;
C;Superfamily: ADP-riboseylation factor
C;Keywords: GTP binding; nucleotide binding; P-loop
F;27-34/Region: nucleotide-binding motif A (P-loop)
F;129-132/Region: GTP-binding NKXD motif

Query Match 85.2%; Score 850.5; DB 2; Length 193;
Best Local Similarity 82.3%; Pred. No. 3.4e-67;
Matches 156; Conservative 20; Mismatches 13; Indels 1; Gaps 1;

QY 1 MFLVDMFYGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGQHOPQYPTSEELS 60
DB 1 MFLVDMFYGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLVQHOPQYPTSEELS 60
QY 61 INRVKFAFDLGGHTTARRVWRDYAKVDALVYLVDAVDRERFESKKEIDSLSDSL 120
DB 61 IGKIKFAFDLGGHQAIRRVWRDYAKVDALVYLVDAVDRERFESKKEIDSLSDSL 120

Db 61 IGIKFKAFDLOGHQIARRVWKDYAKVDVAVVYLVDAYDKERPAESKKEIDALLSDSEALA 120
QY 121 QVPLVVGKNIIDIPYASSEDELRFTTGLT-MTTGKGVNLGDSNIRPIEFVFCISYVRKMG 179
Db 121 TVPPLTGNKIDIPYASSEDELRHGLGTLNFTTGKGVNLGDSGVRLPEVFCISYVRKMG 180
QY 180 YGEGFKMTQYI 191
Db 181 YGEGFKMTQYI 192

RESULT 6

small GTP-binding protein Bearia [imported] - turnip
T52094
C/Species: Brassica rapa (turnip)
C/Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
C/Accession: T52094
R/Kim, W.Y.; Cheong, N.E.; Je, D.Y.; Kim, M.G.; Lim, C.O.; Bahk, J.D.; Cho, M.J.; Lee, S.
Plant Mol. Biol. 33, 1025-1035, 1997
A/Title: The presence of a Sar1 gene family in Brassica campestris that suppresses a yeast
A/Reference number: Z07935
A/Accession: T52094
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-193 <KIM>
A/Cross-references: UNIPROT:O04266; UNIPARC:UPI0000135566; EMBL:U55035; P1DN:AA049716.1
C/Genetics:
A/Gene: Bearia
C/Superfamily: ADP-ribosylation factor

Query Match 85.0%; Score 848.5; DB 2; Length 193;
Best Local Similarity 81.9%; Pred. No. 5,1e-67;
Matches 158; Conservative 22; Mismatches 12; Indels 1; Gaps 1;
QY 1 MFLVDFYFGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGCHOPTQYPTSEELS 60
Db 1 MFLVDFYFGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGCHOPTQYPTSEELS 60
QY 61 INRVKFAFDLGGHTTARRVWRDYAKVDVAVVYLVDAYDKERPAESKKEIDALLSDSELS 120
Db 61 IGIKFKAFDLOGHQIARRVWKDYAKVDVAVVYLVDAYDKERPAESKKEIDALLSDSELS 120
QY 121 QVPLVVGKNIIDIPYASSEDELRFTTGLT-MTTGKGVNLGDSNIRPIEFVFCISYVRKMG 179
Db 121 TVPPLTGNKIDIPYASSEDELRHGLGTLNFTTGKGVNLGDSGVRLPEVFCISYVRKMG 180
QY 180 YGEGFKMTQYI 192
Db 181 YGEGFKMTQYI 193

RESULT 7

T52095
ras-like small monomeric GTP-binding protein [imported] - wild oat
C/Species: Avena sativa (wild oat)
C/Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
C/Accession: T52095
R/Cranston, H.J.; Johnson, R.R.; Chaverra, M.E.; Dyer, W.E.
Plant Sci. 145, 75-81, 1999
A/Title: Isolation and characterization of a cDNA encoding a ras-like monomeric GTP-bind
A/Reference number: Z25949
A/Accession: T52095
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-193 <CRA>
A/Cross-references: UNIPROT:O81695; UNIPARC:UPI000009EBA3; EMBL:AF084005; P1DN:AA032610.
A/Experimental source: cultivar ANZ65
C/Genetics:
A/Gene: SAK1
C/Superfamily: ADP-ribosylation factor

Query Match 84.5%; Score 843.5; DB 2; Length 193;
Best Local Similarity 81.8%; Pred. No. 1.4e-66;

Matches 157; Conservative 22; Mismatches 12; Indels 1; Gaps 1;
QY 1 MFLVDFYFGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGCHOPTQYPTSEELS 60
Db 1 MFLVDFYFGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGCHOPTQYPTSEELS 60
QY 61 INRVKFAFDLGGHTTARRVWRDYAKVDVAVVYLVDAYDKERPAESKKEIDALLSDSELS 120
Db 61 IGIKFKAFDLOGHQIARRVWKDYAKVDVAVVYLVDAYDKERPAESKKEIDALLSDSELS 120
QY 121 QVPLVVGKNIIDIPYASSEDELRFTTGLT-MTTGKGVNLGDSNIRPIEFVFCISYVRKMG 179
Db 121 TVPPLTGNKIDIPYASSEDELRHGLGTLNFTTGKGVNLGDSGVRLPEVFCISYVRKMG 180
QY 180 YGEGFKMTQYI 191
Db 181 YGEGFKMTQYI 192

RESULT 8

T16993
GTP-binding protein Sar1, pollination-induced - apple tree
C/Species: Malus domestica (apple tree)
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C/Accession: T16993
R/Dong, Y.H.; Kvarnheden, A.; Yao, J.L.; Sutherland, P.; Atkinson, R.; Morris, B.; Gardn
submitted to the EMBL Data Library, February 1998
A/Description: Identification of pollination-induced genes from the ovary of apple.
A/Reference number: Z18639
A/Accession: T16993
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-193 <DON>
A/Cross-references: UNIPROT:O65007; UNIPARC:UPI00000AC93D; EMBL:AF048825; NID:g2935451; I
A/Experimental source: cv. Granny Smith; fruit
C/Superfamily: ADP-ribosylation factor
C/Keywords: GTP binding; nucleotide binding; P-loop
P;27-34/Region: nucleotide-binding motif A (P-loop)
F;129-132/Region: GTP-binding NKXD motif

Query Match 83.7%; Score 835.5; DB 2; Length 193;
Best Local Similarity 81.9%; Pred. No. 7e-66;
Matches 158; Conservative 18; Mismatches 16; Indels 1; Gaps 1;
QY 1 MFLVDFYFGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGCHOPTQYPTSEELS 60
Db 1 MFLVDFYFGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGCHOPTQYPTSEELS 60
QY 61 INRVKFAFDLGGHTTARRVWRDYAKVDVAVVYLVDAYDKERPAESKKEIDALLSDSELS 120
Db 61 IGIKFKAFDLOGHQIARRVWKDYAKVDVAVVYLVDAYDKERPAESKKEIDALLSDSELS 120
QY 121 QVPLVVGKNIIDIPYASSEDELRFTTGLT-MTTGKGVNLGDSNIRPIEFVFCISYVRKMG 179
Db 121 AVPLVVGKNIIDIPYASSEDELRHGLGTLNFTTGKGVNLGDSGVRLPEVFCISYVRKMG 180
QY 180 YGEGFKMTQYI 192
Db 181 YGEGFKMTQYI 193

RESULT 9

T16966
GTP-binding protein (clone Np50SAR) - curled-leaved tobacco
C/Species: Nicotiana glauca (curled-leaved tobacco)
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C/Accession: T16966
R/Borisejuk, N.
submitted to the EMBL Data Library, September 1996
A/Reference number: Z18620
A/Accession: T16966
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA

A;Residues: 1-194 <BOR>
A;Cross-references: UNIPROT:O24113; UNIPARC:UPI00000A178F; EMBL:Y08424
C;Superfamily: ADP-ribosylation factor
C;Keywords: GTP binding; nucleotide binding; P-loop
P:27-34/Region: nucleotide-binding motif A (P-loop)
F:129-132/Region: GTP-binding NKXD motif

Query Match 83.4%; Score 832; DB 2; Length 194;
Best Local Similarity 80.3%; Pred. No. 1.4e-65;
Matches 157; Conservative 22; Mismatches 13; Indels 2; Gaps 2;

QY 1 MFLVDMFYGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDELGQHOPTQYPTSEELS 60
DB 1 MFLVDMFYGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDELVQHQPOTYPTSEELS 60
QY 61 INRVKFAFDLGGHTIARRVWDYAKVDIVLVDAVDERFPAESKKELDLSDLS 120
DB 61 IGRKIFAFDLGGHTIARRVWDYAKVDIVLVDAVDERFPAESKKELDLSDLSLA 120
QY 121 QVPVLVGNKIDIPYASSEDELRFGLT-MTTGKGVNLGDSNIRPIEVMCSIVRMKG 179
DB 121 TVPFLIIGNKIDIPYASSEDELRFYOMGLTGTITGKGKVNLAESVVRPLEVFMCSIVRMKG 180
QY 180 -YGEGRKMTQYIK 192
DB 181 IMAGFKRMVSOYIK 194

RESULT 10

hypothetical protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: D86224
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federapfel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maltl, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Ventner, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: D86224

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-193 <STO>
A;Cross-references: UNIPROT:O80489; UNIPARC:UPI000009E5A2; GB:AEO05172; NID:G3249104; P1
C;Genetics:
A;Map position: 1
C;Superfamily: ADP-ribosylation factor

Query Match 82.4%; Score 822.5; DB 2; Length 193;
Best Local Similarity 80.3%; Pred. No. 9.6e-65;
Matches 155; Conservative 20; Mismatches 17; Indels 1; Gaps 1;

QY 1 MFLVDMFYGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDELGQHOPTQYPTSEELS 60
DB 1 MFLVDMFYGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDELVQHQPOTYPTSEELS 60
QY 61 INRVKFAFDLGGHTIARRVWDYAKVDIVLVDAVDERFPAESKKELDLSDLS 120
DB 61 IGRKIFAFDLGGHTIARRVWDYAKVDIVLVDAVDERFPAESKKELDLSDLSLA 120
QY 121 QVPVLVGNKIDIPYASSEDELRFGLT-MTTGKGVNLGDSNIRPIEVMCSIVRMKG 179
DB 121 NVPCIIIGNKIDIPYASSEDELRFYGLTNTFTTGKGINLSDSGVRPLEVFMCSIVRMKG 180
QY 180 YGEGRKMTQYIK 192
DB 181 YGEGRKMTQYIK 193

RESULT 11

T03696

GTP-binding protein SAR1 - common tobacco

C;Species: Nicotiana tabacum (common tobacco)

C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004

C;Accession: T03696

R;Shen, W.H.; Glogot, C.

submitted to the EMBL Data Library, May 1996

A;Description: GTP-binding protein SAR1 of Nicotiana tabacum.

A;Reference number: Z15020

A;Accession: T03696

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-198 <SHE>

A;Cross-references: UNIPROT:P52885; UNIPARC:UPI0000135562; EMBL:X97967; NID:G1340114

A;Experimental source: strain Bright Yellow 2

C;Genetics:

A;Gene: SAR1

C;Superfamily: ADP-ribosylation factor

C;Keywords: GTP binding; nucleotide binding; P-loop

F:27-34/Region: nucleotide-binding motif A (P-loop)

Query Match 70.7%; Score 706; DB 2; Length 198;

Best Local Similarity 70.2%; Pred. No. 1.6e-54;

Matches 139; Conservative 22; Mismatches 31; Indels 6; Gaps 3;

QY 1 MFLVDMFYGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDELGQHOPTQYPTSEELS 60
DB 1 MFLVDMFYGLATLGLMQKEAKILFLGLDNAGKTTLLHMLKDELVQHQPOTYPTSEELS 60
QY 61 INRVKFAFDLGGHTIARRVWDYAKVDIVLVDAVDERFPAESKKELDLSDLS 120
DB 61 IGRKIFAFDLGGHTIARRVWDYAKVDIVLVDAVDERFPAESKKELDLSDLSLA 120
QY 121 QVPVLVGN--KIDIPYAS-SEDELRFGLTMT--GKGVNLGDSNIRPIEVMCSIV 174
DB 121 AHCFLEFLDMNVVTRIRHICCLRRQNRVHGANGASPLARKVNLDSNVRPVEVMCSIV 180
QY 175 VRRKGVGEGRKMTQYIK 192
DB 181 VRRKGVGEGRKMTQYIK 198

RESULT 12

S28605

GTP-binding protein - fission yeast (Schizosaccharomyces pombe)

C;Species: Schizosaccharomyces pombe

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004

C;Accession: S28605; T40209

R;Infert, C.; Genese, M.; Galliard, C.

EMBO J. 11, 4205-4211, 1992

A;Title: Fission yeast and a plant have functional homologues of the Sar1 and Sec12 prote

A;Reference number: S28605; MUID:93011016; PMID:1396601

A;Accession: S28605

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-190 <ENF>

A;Cross-references: UNIPROT:Q01475; UNIPARC:UPI0000135561; GB:M55797; NID:G173397; PIDN:J

R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Pohl, T.

submitted to the EMBL Data Library, August 1997

A;Reference number: Z21913

A;Accession: T40209

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-190 <WOO>

A;Cross-references: UNIPARC:UPI0000135561; EMBL:Z97204; PIDN:CAB10083.1; GSPDB:GN00067; E

A;Experimental source: strain 972h-; cosmid c31f10

C;Genetics:

A;Gene: SPBC31F10.06c

A;Map position: 2

A;Intons: 41/3; 77/1

[illegible]

Oy	177	KMGYGEFGKMTQYI	191
	:		
			:
Db	183	RGYGEFGFWLSQYI	197

Search completed: December 9, 2005, 01:38:41
Job time : 39 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 9, 2005, 01:10:11 ; Search time 158 Seconds
(without alignments)
857.351 Million cell updates/sec

Title: US-10-688-481-11

Perfect score: 998

Sequence: 1 MFLVDMFYGRLASIGLMOKE.....SIVRKMGYGRGFKMTQYIK 192

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 05.80:*
1: uniprot_sprot:*
2: uniprot_tramb1:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	876.5	87.8	193	06PLR8_MAIZE	O6PLR8 zea mays (m
2	872.5	87.3	193	09SDM4_ORYSA	O9SDM4 oryza sativ
3	871.5	87.3	193	09SDM5_TOBAC	O9SDM5 nicotiana t
4	863.5	86.4	193	SAR2_LYCES	P52884 lycopersico
5	862.5	86.4	193	SAR1A_ARATH	O04834 arabidopsis
6	854.5	85.6	193	024110_NICPL	O24110 nicotiana p
7	853.5	85.5	193	08VYP7_ARATH	O8VYP7 arabidopsis
8	852.5	85.4	193	093W16_ORYSA	O93W16 oryza sativ
9	850.5	85.2	193	SAR1B_ARATH	O01474 arabidopsis
10	848.5	85.0	193	SAR1A_BRACM	O04266 brassica ca
11	847.5	84.9	193	024138_TOBAC	O24138 nicotiana t
12	843.5	84.5	193	081695_AVEFA	O81695 avena fatua
13	835.5	83.7	193	065007_MALDO	O65007 malus domes
14	832	83.4	194	024113_NICPL	O24113 nicotiana p
15	831.5	83.3	195	SAR1B_BRACM	O04266 brassica ca
16	822.5	82.4	193	080489_ARATH	O80489 arabidopsis
17	776.5	77.8	194	067UH2_ORYSA	O67UH2 oryza sativ
18	758	76.0	193	061VCL_ORYSA	O61VCL oryza sativ
19	706	70.7	198	SAR1_TOBAC	P52885 nicotiana t
20	674.5	67.6	193	09VD29_DROME	O9VD29 drosophila
21	657.5	65.9	193	07P019_ANOGA	O7P019 anopheles g
22	657	65.8	189	05KM05_CRYNE	O5KM05 cryplococcu
23	657	65.8	189	055X77_CRYNE	O55X77 cryplococcu
24	655	65.6	191	08H713_PHYIN	O8H713 phytophor
25	644	64.5	189	04P017_USTMA	O4P017 ustilago ma
26	641.5	64.3	190	06CB54_YARLI	O6CB54 yarrowia li
27	635	63.6	192	05XU46_9HEMI	O5XU46 xanthopora c
28	628.5	63.0	190	SAR1_SCHPO	O01475 schizosacch
29	627	62.8	189	04WJ57_ASPFU	O4WJ57 aspergillus
30	627	62.8	189	041812_GIBZE	O41812 gibberella
31	625.5	62.7	188	0559R0_DICDI	O559R0 dictyosteli

32	625	62.6	140	2	Q0463_TOBAC	Q0463 nicotiana t
33	625	62.6	189	2	O877B9_ASPOR	O877B9 aspergillus
34	623	62.4	189	1	SAR1_TRIRE	P78976 trichoderma
35	622.5	62.4	211	2	O5CVH4_CRYPV	O5CVH4 cryptospori
36	621.5	62.3	197	2	O9NFB8_DROME	O9NFB8 drosophila
37	621.5	62.3	198	2	O567Y5_BRARE	O567Y5 brachydanio
38	621	62.2	189	2	O5BGB9_EBENI	O5BGB9 espergilliu
39	620.5	62.2	193	2	O5CKN9_CRYHO	O5CKN9 cryptospori
40	619.5	62.1	190	1	SAR1_PICPA	O9P468 pictia past
41	619	62.0	189	2	O5EMZ6_MAGCR	O5EMZ6 magnaporthe
42	619	62.0	189	2	O52BE4_MAGCR	O52BE4 magnaporthe
43	616.5	61.8	198	1	SAR1B_MOUSE	O9CG9 mus muscula
44	615.5	61.7	198	2	Q4ZJK0_PIG	Q4ZJK0 sus scrofa
45	614.5	61.6	198	1	SAR1B_CRIGR	O9QVY3 cricetus

ALIGNMENTS

RESULT 1									
ID	06PLR8_MAIZE	PRELIMINARY;	PRT;	193 AA.					
AC	06PLR8;								
DT	05-JUL-2004 (TREMBLrel. 27, Created)								
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)								
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)								
DE	Putative ras-like small GTP binding protein.								
OS	Zea mays (Maize).								
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;								
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;								
OC	PACCAD clade; Panicoidae; Andropogoneae; Zea.								
OX	NCBI_TaxID=4577;								
RN	[1]								
RP	NUCLEOTIDE SEQUENCE.								
RA	Zhang Z., Tang W., Zheng Y.;								
RL	Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.								
DR	EMBL: AY596178; AAT06576.1; -, mRNA.								
DR	GO: GO:0005794; C:Golgi apparatus; IEA.								
DR	GO: GO:0005525; F:GTP binding; IEA.								
DR	GO: GO:0006886; P:intracellular protein transport; IEA.								
DR	GO: GO:0007264; P:small GTPase mediated signal transduction; IEA.								
DR	InterPro: IPR006689; ARF.								
DR	InterPro: IPR001806; Ras_trnsfmg.								
DR	InterPro: IPR006687; SAR1.								
DR	InterPro: IPR005225; Small_GTP.								
DR	Pfam: PF00025; Arf; 1.								
DR	PRINTS: PR00449; RASTRNSFRMG.								
DR	PRINTS: PR00328; SAR1GTPBP.								
DR	SMART: SM00177; ARF; 1.								
DR	SMART: SM00178; SAR; 1.								
DR	TIGRFAMs: TIGR00231; small_GTP; 1.								
DR	TIGRFAMs: TIGR00231; small_GTP; 1.								
DR	SEQUENCE 193 AA; 22012 MW; EF9167BD74E2DF68 CRC64;								
QY	Query Match	87.8%;	Score 876.5;	DB 2;	Length 193;				
QY	Best Local Similarity	83.9%;	Pred. No. 7e-65;						
QY	Matches 162;	Conservative 20;	Mismatches 10;	Indels 1;	Gaps 1;				
QY	1	MFLVDMFYGRLASIGLMOKEAKILFLGLDNAGKTTLLHMLKDEKLGOHPTQPTSELS	60						
Db	1	MFLVDMFYGVLASIGLMOKEAKILFLGLDNAGKTTLLHMLKDEKLVOHPTQPTSELS	60						
QY	61	INRYKFAFDLGGHTTIRARWRDYAAVDAIVYLVDAVDREPRASEKKEIDSLSDSLS	120						
Db	61	IGRIKFAFDLGGHTTIRARWRDYAAVDAIVYLVDAVDKERFASKEKEDALLADDSLA	120						
QY	121	QVPLVVGNNKIDIPYASSEDLRPTGLT-MTGGKGTVNLGDSNIRPIEFVFCISVRRMG	179						
Db	121	NVPLFLGNKIDIPYASSEDLRPTGLT-MTGGKGTVNLGDSNIRPIEFVFCISVRRMG	180						
QY	180	YGBGFKMTQYIK 192							
Db	181	YGBGFKMTQYIK 193							

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RESULT 2
Q9SDK4_ORYSA
AC Q9SDK4_
ID Q9SDK4_ORYSA PRELIMINARY; PRT; 193 AA.
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Putative small GTP-binding protein Baxria (GTP-binding protein).
GN Name=PO705D01.9; Synonyms=GBP;
OS Oryza sativa (Japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsunoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
RA Wu J., Nilmura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
RA Hosokawa S., Maekawa M., Arikawa K., Chiden Y., Hayashi M.,
RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
RA Higashita S., Honda S., Itoh T., Itoh Y., Itonuma A., Iijima M., Ikeda M.,
RA Ikano M., Itoh S., Itoh T., Itoh Y., Iwabuchi A., Kamiya K.,
RA Karasawa M., Katagiri S., Kikuta A., Kodayashi N., Kono I.,
RA Mochita K., Maehara T., Mizuno H., Mizubayashi Y., Nakamura M.,
RA Nagasaka H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,
RA Shimokawa T., Shomura A., Song J., Takasaki Y., Terasawa K., Tsuji K.,
RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
RA Zhang H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
RA Yano M., Jiang J., Gojobori T.;
RT "The genome sequence and structure of rice chromosome 1.";
RL Nature 420:312-316(2002).
[2]
RP NUCLEOTIDE SEQUENCE.
RA Meng X.-B., Lin R.-M., Wang M., Zhao W.-S., Peng Y.-L.;
RL Submitted (APR-2004) to the EMBL/Genbank/DBJ databases.
CC -1 SIMILARITY: Belongs to the small GTPase superfamily.
DR EMBL; AF000492; BAAB4612.1; -; Genomic_DNA.
DR EMBL; AY620417; AAT28677.1; -; mRNA.
DR HSSP; Q9OYV3; 1F6B.
DR Gramene; Q9SDK4; -.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0006886; P:intracellular protein transport; IEA.
DR GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.
DR InterPro; IPR006689; ARF/SAR.
DR InterPro; IPR001806; Ras_transfmrng.
DR InterPro; IPR006687; SAR1_GTP_bd.
DR InterPro; IPR005225; Small_GTP_bd.
DR Pfam; PF00025; Arf; 1.
DR PRINTS; PR00429; RASTRNSFRMNG.
DR PRINTS; PR00328; SAR1GTPBP.
DR SMART; SM00178; SAR; 1.
DR TIGRFAMs; TIGR00231; small_GTP; 1.
DR KEGG; gtp-binding; Nucleotide-binding.
SQ SEQUENCE 193 AA; 21944 MW; BCAC934283DECFT8 CRC64;

Query Match 87.4%; Score 872.5; DB 2; Length 193;
Best Local Similarity 83.4%; Pred. No. 1.5e-64;
Matches 161; Conservative 20; Mismatches 11; Indels 1; Gaps 1;

Qy 1 MFLVDMFYGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGQHPTQPTSEELS 60
Db 1 MFLVDMFYGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGQHPTQPTSEELS 60

Qy 61 INRYKFAFDLGGTTIARRVRWDYARVDAIVYLVDAVDERPFAESKKEIDSLSDSL 120
Db 61 IGIKIFKAFDGGQIARRVKWDYARVDAIVYLVDAVDERPFAESKKEIDSLSDSLA 120

Qy 121 QVPLVVGKTKIDIPYASSEDRLRFTLGLT-MTTGKGTVNLGDSNIRPIEFVFMCSIVKMG 179
Db 121 TVPFLILGNKIDIPYASSEDRLRFTLGLT-MTTGKGTVNLGDSNIRPIEFVFMCSIVKMG 180

Qy 121 TVPFLILGNKIDIPYASSEDRLRFTLGLT-MTTGKGTVNLGDSNIRPIEFVFMCSIVKMG 180

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Qy 180 YGEGFKMTQYIK 192
Db 181 YGEGFKMTQYIK 193

RESULT 3
Q9SD05_TOBAC
ID Q9SD05_TOBAC PRELIMINARY; PRT; 193 AA.
AC Q9SD05_
ID Q9SD05_
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Small GTP-binding protein Sar1BNL.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; Lamiales; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Tissue= Mature leaves;
RA Andreeva A.V., Kutuzov M.A., Evans D.E., Hawes C.R.;
RL Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.
CC -1 SIMILARITY: Belongs to the small GTPase superfamily.
DR EMBL; AF210431; AAF17254.1; -; mRNA.
DR PIR; T52096; T52096.
DR HSSP; Q9OYV3; 1F6B.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0006886; P:intracellular protein transport; IEA.
DR GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.
DR InterPro; IPR006689; ARF/SAR.
DR InterPro; IPR001806; Ras_transfmrng.
DR InterPro; IPR006687; SAR1_GTP_bd.
DR InterPro; IPR005225; Small_GTP_bd.
DR Pfam; PF00025; Arf; 1.
DR PRINTS; PR00449; RASTRNSFRMNG.
DR PRINTS; PR00328; SAR1GTPBP.
DR SMART; SM00178; SAR; 1.
DR TIGRFAMs; TIGR00231; small_GTP; 1.
DR PROSITE; PS01020; SAR1; 1.
DR KEGG; gtp-binding; Nucleotide-binding.
SQ SEQUENCE 193 AA; 22010 MW; 118CF5894EB6BF4E CRC64;

Query Match 87.3%; Score 871.5; DB 2; Length 193;
Best Local Similarity 83.4%; Pred. No. 1.8e-64;
Matches 161; Conservative 21; Mismatches 10; Indels 1; Gaps 1;

Qy 1 MFLVDMFYGLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGQHPTQPTSEELS 60
Db 1 MFLVDMFYGLATIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGQHPTQPTSEELS 60

Qy 61 INRYKFAFDLGGTTIARRVRWDYARVDAIVYLVDAVDERPFAESKKEIDSLSDSL 120
Db 61 IGIKIFKAFDGGQIARRVKWDYARVDAIVYLVDSFDERPFAESKKEIDSLSDSLA 120

Qy 121 QVPLVVGKTKIDIPYASSEDRLRFTLGLT-MTTGKGTVNLGDSNIRPIEFVFMCSIVKMG 179
Db 121 TVPFLILGNKIDIPYASSEDRLRFTLGLT-MTTGKGTVNLGDSNIRPIEFVFMCSIVKMG 180

Qy 180 YGEGFKMTQYIK 192
Db 181 YGEGFKMTQYIK 193

RESULT 4
ID SAR2_LYCES
ID SAR2_LYCES STANDARD; PRT; 193 AA.
AC P52884;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE GTP-binding protein SAR2.

```

GN Name=SAR2;
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC Asterids; Lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.
OX NCBI_TaxID=4081;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Pericarp;
RX MEDLINE=94169306; PubMed=8123794;
RA Davies C.;
RT "Cloning and characterization of a tomato GTPase-like gene related to yeast and Arabidopsis genes involved in vesicular transport."
RL Plant Mol. Biol. 24:525-531(1994).
CC - FUNCTION: Involved in transport from the endoplasmic reticulum to the Golgi apparatus (by similarity).
CC - SIMILARITY: Belongs to the small GTPase superfamily, SAR1 family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC
CC EMBL: L12051; AAA34168.1; -; mRNA.
CC PIR: S42528; S42528.
CC HSSP: Q9QVY3; 1P6B.
CC InterPro: IPR006689; ARF/SAR.
CC InterPro: IPR001806; Ras_trnsmfmg.
CC InterPro: IPR006687; SAR1_GTP_bd.
CC InterPro: IPR005225; Small_GTP_bd.
CC PANTHER: PTHR11711; ARF/SAR; 1.
CC Pfam: PF000025; Arf; 1.
CC PRINTS: PR00449; RASTRNSFRMG.
CC PRINTS: PR00328; SAR1GTPB.
CC SMART: SM00178; SAR; 1.
CC TRIFRAMS: TRG00231; small_GTP; 1.
CC PROSITE: PS01020; SAR1; 1.
CC Endoplasmic reticulum; ER-Golgi transport; Golgi stack; GTP-binding;
CC Nucleotide-binding; Protein transport; Transport.
CC NP_BIND 27 GTP (By similarity).
CC FT NP_BIND 70 GTP (By similarity).
CC FT NP_BIND 129 132 GTP (By similarity).
CC FT NP_BIND 129 132 GTP (By similarity).
CC SQ SEQUENCE 193 AA; 21923 MW; CF5223DB9D599BAF CRC64;

Query Match 86.5%; Score 863.5; DB 1; Length 193;
Best Local Similarity 83.9%; Pred. No. 8.5e-64;
Matches 162; Conservative 16; Mismatches 14; Indels 1; Gaps 1;

QY 1 MFLVDMFYGLASIGLMQKAKILFLGLDNAGKTTLLHMLKDEKLGQHOPPTSEELS 60
DB 1 MFLVDMFYGLASIGLMQKAKILFLGLDNAGKTTLLHMLKDEKLGQHOPPTSEELS 60
QY 61 INNVKFAKAPLGSHHTARVWRDYAKVDIVYLVDAVDREPERAESKKEGLSLSDSL 120
DB 61 INNVKFAKAPLGSHHTARVWRDYAKVDIVYLVDAVDREPERAESKKEGLSLSDSL 120
QY 61 IGNIKKAPLGSHHTARVWRDYAKVDIVYLVDAVDREPERAESKKEGLSLSDSL 120
DB 61 IGNIKKAPLGSHHTARVWRDYAKVDIVYLVDAVDREPERAESKKEGLSLSDSL 120
QY 121 QVPLVLGNKIDIPYASSEDELRFITGLT-MTTGKGVNLGDSNIRPIEIVMCSIVKMG 179
DB 121 NVFPLILGNKIDIPYASSEDELRFITGLT-MTTGKGVNLGDSNIRPIEIVMCSIVKMG 179
QY 180 YGSGFKMNTQYK 192
DB 180 YGSGFKMNTQYK 192
QY 181 YGSGFKMNTQYK 193
DB 181 YGSGFKMNTQYK 193

DE GTP-binding protein SAR1A.
GN Name=SAR1A; OrderedLocustNames=At4g02080; ORFNames=T10M13.9, AGAA.4;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=cv. Columbia;
RA Winge P., Brembu T., Bones A.M.;
RT Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
RL [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=cv. Columbia;
RX MEDLINE=20083468; PubMed=10617198; DOI=10.1098/47134;
RA Mayer K.F.X., Scheller C., Wambutt R., Murphy G., Volkert G.,
RA Pohl T., Duesterhoeft A., Stiekema W., Ehlman K.-D., Terry N.,
RA Harris B., Anstorge W., Brandt P., Grivell L.A., Rieger M.,
RA Weichselgartner M., de Simone V., Obermayer B., Maché R., Mueller M.,
RA Kreis M., Delzeny M., Püsgdomenech P., Watson M., Schmidheini T.,
RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
RA Vos P., Hohnel J., Zimmermann W., Wedler H., Ridley P.,
RA Langham S.-A., McCullagh B., Bilham L., Robben J.,
RA Van der Schueren J., Grymoprez B., Chuang Y.-J., Vandenbussche F.,
RA Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,
RA Weitzneger T., Botne G., Rampersger U., Hilbert H., Braun M.,
RA Holzner E., Brandt A., Peters S., van Staeren M., Dirke W.,
RA Woolfman P., Klein Lankhorst R., Rose M., Hauf J., Koelter P.,
RA Bernsleier S., Hempel S., Feldpausch M., Lambert S., Van den Daele H.,
RA De Keyser A., Buyschaert C., Gielen J., Villarroel R., De Clercq R.,
RA Van Montagu M., Rogers J., Cronin A., Quall M.A., Bray-Allen S.,
RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McIay K., Mayes R.,
RA Peetec A., Rajandream M.A., Lyne M., Benes V., Reckmann S.,
RA Borkova D., Bloecker H., Scharfe M., Grimm M., Loehner T.-H.,
RA Dose S., de Haan M., Marase A.C., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fartmann B., Granderach K., Dauner D., Herzl A.,
RA Neumann O., Ariglou A., Vitale D., Liguori R., Piravadi B.,
RA Messner S., Orsigh F., Schmidt W., Lechary A., Aubourg S.,
RA Schenkl S., Hiller R., Schmidt W., Lechary A., Aubourg S.,
RA Gibson F., Cooke R., Berger C., Montfort A., Casacuberta E.,
RA Chibbons T., Weber N., Vandenbol M., Bargues M., Terol J., Torres A.,
RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Taccon D., Jesse T.,
RA Heijnen L., Schwarz S., Scholler P., Heber S., Frances P., Bielke C.,
RA Frisman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Zaccaria P., Bevan M., Wilson R.K., de la Baetide M., Habermann K.,
RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
RA Skonking T., Kalicki J., Graves T., Harmon G., Edwards J.,
RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Mink P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.W.,
RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Jochu C.,
RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Ma P., Zhong J., Preston R., Vil D., Sheker M., Macero A., Shah R.,
RA Saby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
RA Grant S., Shohdy N., Hasegawa A., Hameed A., Lodi M., Johnson A.,
RA Chen E., Maria M.A., Martienssen R., McCormie W.R.;
RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana."
RL Nature 402:769-777(1999).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=cv. Landsberg erecta;
RA Till S., Grant S., Parnell L., Kaplan N., Hoffman J., Lodi M.,
RA Johnson A.F., Dedhia N., Martienssen R., McCormie W.R.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=cv. Columbia;
RX MEDLINE=22954850; PubMed=14593172; DOI=10.1126/science.1086305;
RA Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,

RA Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
RA Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
RA Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Tortum M.J.,
RA Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Anseri Y.,
RA Arawaka T., Banh J., Bamco F., Bowser L., Brooks S.Y., Carinci P.,
RA Chao Q., Choy N., Enju A., Goldenrich A.D., Gurjal M., Hansen N.F.,
RA Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Kanes M.,
RA Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,
RA Kamliya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,
RA Satou M., Tame R., Vaynsberg M., Wallender E.K., Wong C., Yamamura Y.,
RA Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RT "Empirical analysis of transcriptional activity in the Arabidopsis
genome.";
RL Science 302:842-846(2003).
RN [5]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RA Brover V., Trounhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.A.;
RT "Full-length cDNA from Arabidopsis thaliana.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 104-193.
RC STRAIN=Cy. Columbia; TISSUE=seedling;
RX MEDLINE=36159348; PubMed=8580968;
RX DOI=10.1046/j.1365-3113.1996.09010101.x;
RA Cooke R., Raynal M., Laudie M., Grellet F., Delzeny M., Morris P.-C.,
RA Guerrier D., Giraudat J., Guigley F., Chabault G., Li Y.-F., Maché R.,
RA Krivitzky M., Gy I.J.-J., Kreis M., Lecharny A., Parmentier Y.,
RA Marbach J., Fleck J., Clement B., Philippe G., Hervé C., Bardet C.,
RA Tremoussaye D., Lescure B., Lacomme C., Roby D., Jourjon M.-F.,
RA Chabrier P., Charpentier J.-L., Desprez T., Anselme J., Chappellet H.,
RA Hoeft H.;
RT "Further progress towards a catalogue of all Arabidopsis genes:
RT analysis of a set of 5000 non-redundant ESTs.";
RL Plant J. 9:101-124(1996).
RN [1]
RP FUNCTION: Involved in transport from the endoplasmic reticulum to
the Golgi apparatus (By similarity).
CC -1- SIMILARITY: Belongs to the small GTPase superfamily. SAR1 family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL: U56929; AAA93827.1; -; mRNA.
DR EMBL: AF001308; AAC78700.1; -; Genomic DNA.
DR EMBL: AL161483; CAB80701.1; -; Genomic DNA.
DR EMBL: AF001535; AAB57799.1; -; Genomic DNA.
DR EMBL: AY065357; AAL38798.1; -; mRNA.
DR EMBL: AY066699; AAM20333.1; -; mRNA.
DR EMBL: AY088765; AAM67080.1; -; mRNA.
DR EMBL: Z26707; CAA81406.1; -; mRNA.
DR PIR: T01509; T01509.
DR HSSP: Q9QVY3; 1F6B.
DR InterPro: IPR006689; ARF/SAR.
DR InterPro: IPR001806; Ras trnsfmg.
DR InterPro: IPR006687; SAR1 GTP bd.
DR InterPro: IPR005225; Small GTP bd.
DR PANTHER: PTHR11711; ARF/SAR; 1.
DR Pfam: PF00025; Arf; 1.
DR PRINTS: PR00449; RASTRNSFRMG.
DR PRINTS: PR00328; SAR1GTPBP.
DR SMART: SM00178; SAR; 1.
DR TIGRFAMs: TIGR00231; small_GTP; 1.
DR PROSITE: PS01020; SAR1; 1.
KW Endoplasmic reticulum; ER-Golgi transport; Golgi stack; GTP-binding;
KW Nucleotide-binding; Protein transport; Transport.
FT NP_BIND 27 34 GTP (By similarity).
FT NP_BIND 70 73 GTP (By similarity).
FT NP_BIND 129 132 GTP (By similarity).
SQ SEQUENCE 193 AA; 22030 MW; 641D1664548A0BE CRC64;

Query Match 86.4%; Score 862.5; DB 1; Length 193;
Best Local Similarity 82.4%; Pred. No. 1e-63;
Matches 160; Conservative 21; Mismatches 11; Indels 1; Gaps 1;
QY 1 MFLVDFYFGYGLASIGLMQKEAKILFLGLDAGKTTLLHMLKDEKLGQHOPQTOYPTSELS 60
DB 1 MFLVDFYGLVSLGLQKAKILFLGLDAGKTTLLHMLKDEKRLVQHOPQTOYPTSELS 60
QY 1 INRKFAFDLGHTTARRVWRDYAKVDAIVYLVDVDERPAESKKEIDSLSDSLS 120
DB 1 IGKIKFAFDLGHTTARRVWRDYAKVDAIVYLVDVDERPAESKKEIDSLSDSLS 120
QY 121 QVPLVLTGNKIDIPYASSEDELRFITGLT-MTTGKGTVNLGDSNIRPIEFVMSIVKMG 179
DB 121 SVPLLTGNKIDIPYASSEDELRFITGLTSGFTTGKRVNLDSNVRPLEVFMCSIVKMG 180
QY 180 YGEFGKMTQYIK 192
DB 181 YGEFGKMTQYIK 193
RESULT 6
ID 024110_NICPL PRELIMINARY; PRT; 193 AA.
AC 024110;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Small GTP-binding protein.
OS Nicotiana glauca (Leadwort-leaved tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliopsida; eudicotyledons; core eudicotyledons;
OC asterids; lamiales; Solanales; Solanaceae; Nicotiana.
OX NCBI_Taxid=4092;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Borisyuk N.;
RT Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the small GTPase superfamily.
DR EMBL: Y08423; CAA69699.1; -; mRNA.
DR PIR: T16964; T16964.
DR HSSP: Q9QVY3; 1F6B.
DR GO: GO:0005525; F:GTP binding; IEA.
DR GO: GO:0006886; P:intracellular protein transport; IEA.
DR GO: GO:0007264; P:small GTPase mediated signal transduction; IEA.
DR InterPro: IPR006689; ARF/SAR.
DR InterPro: IPR001806; Ras trnsfmg.
DR InterPro: IPR006687; SAR1 GTP bd.
DR InterPro: IPR005225; Small GTP bd.
DR Pfam: PF00025; Arf; 1.
DR PRINTS: PR00449; RASTRNSFRMG.
DR PRINTS: PR00328; SAR1GTPBP.
DR SMART: SM00178; SAR; 1.
DR TIGRFAMs: TIGR00231; small_GTP; 1.
DR PROSITE: PS01020; SAR1; 1.
KW GTP-binding; Nucleotide-binding.
SQ SEQUENCE 193 AA; 21935 MW; F2718819740F506E CRC64;
Query Match 85.6%; Score 854.5; DB 2; Length 193;
Best Local Similarity 82.4%; Pred. No. 4.8e-63;
Matches 159; Conservative 21; Mismatches 12; Indels 1; Gaps 1;
QY 1 MFLVDFYFGYGLASIGLMQKEAKILFLGLDAGKTTLLHMLKDEKLGQHOPQTOYPTSELS 60
DB 1 MFLVDFYGLVSLGLQKAKILFLGLDAGKTTLLHMLKDEKRLVQHOPQTOYPTSELS 60
QY 1 INRKFAFDLGHTTARRVWRDYAKVDAIVYLVDVDERPAESKKEIDSLSDSLS 120
DB 1 IGKIKFAFDLGHTTARRVWRDYAKVDAIVYLVDVDERPAESKKEIDSLSDSLS 120
QY 121 QVPLVLTGNKIDIPYASSEDELRFITGLT-MTTGKGTVNLGDSNIRPIEFVMSIVKMG 179
DB 121 TVPLLTGNKIDIPYASSEDELRFITGLTGVTTGKRVNLDSNVRPLEVFMCSIVKMG 180

QY	180	YGEGFKNMTQYIK 192
	181	YGDGFKWVSQYIK 193
Db		
RESULT 7		
Q8VYP7_ARATH		
Q8VYP7_ARATH PRELIMINARY;	PRT;	193 AA.
AC Q8VYP7		
DT 01-MAR-2002 (TREMBLrel. 20, Created)		
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)		
DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)		
DE Putative Sar1 GTP binding protein.		
GN Name=A3362550;		
OS Arabidopsis thaliana (mouse-ear cress).		
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;		
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.		
OC NCBI_TaxID=3702;		
RN [1]		
RP NUCLEOTIDE SEQUENCE.		
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,		
RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,		
RA Garinaci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,		
RA Kamuya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,		
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,		
RA Seki M., Shim P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,		
RA Theologis A.;		
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.		
RN [2]		
RP NUCLEOTIDE SEQUENCE.		
RA Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,		
RA Tang J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,		
RA Deng C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,		
RA Garinaci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,		
RA Kamuya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,		
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,		
RA Seki M., Shim P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,		
RA Theologis A.;		
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.		
CC -1 SIMILARITY: Belongs to the small GTPase superfamily.		
DR EMBL; AY070378; AA149874.1; -; mRNA.		
DR EMBL; AY117363; AA651438.1; -; mRNA.		
DR HSSP; Q9QY3; 1F6B.		
DR GO; GO:0005525; F:GTP binding; IEA.		
DR GO; GO:0006886; P:intracellular protein transport; IEA.		
DR GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.		
DR InterPro; IPR006689; ARF/SAR.		
DR InterPro; IPR001806; Ras_trnsmfmg.		
DR InterPro; IPR006687; SARI_GTP_bd.		
DR InterPro; IPR005225; Small_GTP_bd.		
DR Pfam; PF000025; Art; 1.		
DR PRINTS; PR00449; RASTRNSFRMNG.		
DR PRINTS; PR00328; SARI_GTPBP.		
DR SMART; SM00178; SAR; 1.		
DR TIGRFAMs; TIGR00231; small_GTP; 1.		
DR PROSITE; PS01020; SARI; 1.		
KW GTP-binding; Nucleotide-binding.		
SC SEQUENCE 193 AA; 21933 MW; AA7D50764B33F848 CRC64;		
Query Match 85.5%; Score 853.5; DB 2; Length 193;		
Best Local Similarity 82.8%; Pred. No. 5; 8e-63;		
Matches 159; Conservative 20; Mismatches 12; Indels 1; Gaps 1		
QY 1 MFLVDMFPGFLASIGLMQGEAKITPLGLDNAGKTTLLHMLKBEKGGQHPOTYPPSEELS 60		
Db 1 MFLVDMFPGFLATLGLMQGEAKITPLGLDNAGKTTLLHMLKBERLWQHPTQHPSEELS 60		
QY 61 INRVKPKAFDGLGSHLTARVWRDYYAKVDAYIVLDAVDVRERPAESKKEKLDLSDLS 120		
Db 61 IKTITFKAFDGLGSHLTARVWRDYYAKVDAYIVLDAVDVRERPAESKKEKLDLSDLS 120		

Qy	121	QVPLVYVGNKIDIPYASSEBDELRTLLGTT-MTTSKGVNLQDSSNIRPLEVMCSIVRQSG	179
Db	121	NWPLILKIDIDIPYASSEBDELRTLLGTTSTTKGVNVLNAGTVRPLEVMCSIVRQSG	180
Qy	180	YGEQGFKNMTOYI 191	
Db	181	YGEQGFKNMTOYI 192	
RESULT 8			
Q93W16	ORYSA		
ID	093W16	ORYSA PRELIMINARY;	PRT; 193 AA.
AC	093W16		
DT	01-DEC-2001	(TrEMBLrel. 19, Created)	
DT	01-DEC-2001	(TrEMBLrel. 19, Last sequence update)	
DT	01-FEB-2005	(TrEMBLrel. 29, Last annotation update)	
DE		Putative small GTP-binding protein Bsaar1a.	
GN	Name=BI08BD01.1; Synonyms=P0487EL1.37;		
OS	Oryza sativa (japonica cultivar-group).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae;		
OC	Ehrhartoideae; Oryzoae; Oryza.		
OX	NCBI_Taxid=39947;		
RP	NUCLEOTIDE SEQUENCE.		
RA	Saeki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,		
RA	Mu Y., Milmura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,		
RA	Hosokawa S., Maekawa M., Arikawa K., Chiden Y., Hayashi M.,		
RA	Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,		
RA	Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,		
RA	Ikeno M., Itoh S., Itoh T., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K.,		
RA	Kanawa W., Katagiri T., Kikuta A., Kodayashi N., Kono I.,		
RA	Maehita K., Maehita T., Mizuno H., Mizubayashi T., Mukai Y.,		
RA	Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,		
RA	Namiki N., Negishi M., Ohta I., Ono N., Saito S., Sakai K., Shibata M.,		
RA	Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,		
RA	Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,		
RA	Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,		
RA	Yano M., Jiang Y., Gojobori T.;		
RL	"The genome sequence and structure of rice chromosome 1.";		
RL	Nature 420:312-316(2002).		
CC	-1- SIMILARITY: Belongs to the small GTPase superfamily.		
DR	EMBL; AP003331; BAB67979.1; -; Genomic_DNA.		
DR	EMBL; AP003793; BAB6877.1; -; Genomic_DNA.		
DR	HSSP; Q9QYV3; 1F6B.		
DR	Gene; G93W16; -.		
DR	GO; GO:0005525; P:GTP binding; IEA.		
DR	GO; GO:0006886; P:intracellular protein transport; IEA.		
DR	GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.		
DR	InterPro; IPR006689; ARF/SAR.		
DR	InterPro; IPR001806; Ras trnsmfmg.		
DR	InterPro; IPR006687; SAR1 GTP bd.		
DR	InterPro; IPR005225; Small_GTP_bd.		
DR	Pfam; PF00025; Arf; 1.		
DR	PRINTS; PRO0449; RASTRNSFRMG.		
DR	PRINTS; PRO0328; SAR1GTPBP.		
DR	SMART; SM00178; SAR; 1.		
DR	TIGRFAMs; TIGR00231; small_GTP; 1.		
DR	PROSITE; PS01020; SAR1; 1.		
DR	GTP-binding; Nucleotide-binding.		
KW	SEQUENCE 193 AA; 21984 MW; 65351FBI8E40BAD9 CRC64;		
SC			
Query Match	85.4%;	Score 852.5;	DB 2; Length 193;
Best Local Similarity	81.9%;	Pred. No. 7e-63;	
Matches 158;	Conservative 23;	Mismatches 11;	Indels 1; Gaps 1
Qy	1	MFLVDFYGFGLASIGLWQKEAKILFLGLDNGKTTLLHMLDKELGQHOPFYPTSEELS	60
Db	1	MFLVDFYGFGLASIGLWQKEAKILFLGLDNGKTTLLHMLDKELRVLQHPOTCHPTSEELS	60
Qy	61	INRYKFKAFDLCGHTIARVRWDYAKADAIYLVYLDVANDRERFAPSKKELDLSDDSL	120
Db	61	IGKIKFKAFDLCGHTIARVRWDYAKADVAVVYLDVADKEKFAESKKELDLSDDSLA	120

QY 121 QVPVLVGNKIDIPYASSEDEBLRFTLGLT-MTGGKGVNIGDSNIRPIEVFMCIVAKMG 179
DB 121 AVPELIIGNKIDIPYASSEELRYHGLISNFTTGKGVNIGDSNIRPIEVFMCIVAKMG 180
QY 180 YGSGFKMTTOYIK 192
DB 181 YGSGFKMTTOYIK 193

RESULT 9
SARIB ARATH STANDARD; PRT; 193 AA.
ID SARIB ARATH
AC 001474;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE GTP-binding protein SARIB.
GN Name=SARIB; Synonyms=SAR1; OrderedLocustNames=At1g56330;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OC NCBI_TaxID=3702;
OX 11
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=93011016; PubMed=1396601;
RX d'Amfert C., Genesee M., Gallardin C.C.;
RT "Fission yeast and a plant have functional homologues of the Sar1 and
Sec12 proteins involved in ER to Golgi traffic in budding yeast.",
RL BMO J. 11:4205-4211(1992).
[2]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=cnv. Columbia;
RX MEDLINE=21016719; PubMed=1130712; DOI=10.1038/35048500;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altati H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Creasy T.H., Dewar K.,
RA Dunn P., Egtu P., Feldlyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin B.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,
RA Miltschker J., Miranda M., Nguyen M., Nieman W.C., Osborne B.I.,
RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Utecherback T., Van Aken S., Vayberg M., Vayotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Ventler J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
thaliana.",
RL Nature 408:816-820(2000).
[3]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RP STRAIN=cnv. Columbia;
RX MEDLINE=22954850; PubMed=14593172; DOI=10.1126/science.1088305;
RA Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,
RA Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
RA Karlin-Newman G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
RA Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
RA Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,
RA Arakawa T., Banh U., Banno F., Bowser L., Brooks S.Y., Carninci P.,
RA Chao Q., Choy N., Egtu A., Goldsmith A.D., Guiral M., Hansen N.F.,
RA Hayashizaki Y., Johnson-Hopson C., Huan V.M., Iida K., Karnes M.,
RA Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,
RA Kamuya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,
RA Satou M., Tame R., Vayberg M., Wallender E.K., Wong C., Yamamura Y.,
RA Yuan S., Shinzaki K., Davis R.W., Theologis A., Ecker J.R.;
RT "Empirical analysis of transcriptional activity in the Arabidopsis
genome.";

RL Science 302:842-846(2003).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RA Brover V., Trukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.A.;
RT "Full-length cDNA from Arabidopsis thaliana.",
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Involved in transport from the endoplasmic reticulum to
CC the Golgi apparatus (By similarity).
CC -1- SIMILARITY: Belongs to the small GTPase superfamily. SAR1 family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL nucleotide
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
DR EMBL; M95795; AAA32807.1; -; mRNA.
DR EMBL; AC069159; AAC50911.1; -; Genomic DNA.
DR EMBL; AY072220; AAL60041.1; -; mRNA.
DR EMBL; AY096559; AAM20249.1; -; mRNA.
DR EMBL; AY085815; AAM63031.1; -; mRNA.
DR PIR; S28603; S28603.
DR HSSP; Q9QVY3; 1P68.
DR InterPro; IPR006689; ARF/SAR.
DR InterPro; IPR001806; Ras_transfmg.
DR InterPro; IPR006687; SAR1_GTP_bd.
DR InterPro; IPR005225; Small_GTP_bd.
DR PANTHER; PTHR11711; ARF/SAR; 1.
DR Pfam; PF00025; Arf; 1.
DR PRINTS; PR00449; RASTRNSPRMG.
DR PRINTS; PR00328; SARIGTPBP.
DR SMART; SM00178; SAR; 1.
DR TIGRFAMs; TIGR00231; small_GTP; 1.
DR PROSITE; PS01020; SAR1; 1.
DR Endoplasmic reticulum; ER-Golgi transport; Golgi stack; GTP-binding;
KM Nucleotide-binding; Protein transport; Transport.
FT NP_BIND 27 34 GTP (By similarity).
FT NP_BIND 70 73 GTP (By similarity).
FT NP_BIND 129 132 GTP (By similarity).
SQ SEQUENCE 193 AA; 21986 MW; 9D9AE86B3E68878 CRC64;
Query Match 85.2%; Score 850.5; DB 1; Length 193;
Best local similarity 82.3%; Pred. No. 1e-62;
Matches 158; Conservative 20; Mismatches 13; Indels 1; Gaps 1;
QY 1 MELVDWVFYGLASIGLQKAKILFLGLDNAGKTTLLHMLKDEKLGQHOPTOYPTSELS 60
DB 1 MFLFDWVFYGLASIGLQKAKILFLGLDNAGKTTLLHMLKDEKLVQHOPTOYPTSELS 60
QY 61 INRYKFAFPLDGGHTTARRVWDYAKVDAIVLVDAVDERPAESKKELDLSLSDLS 120
DB 61 IGKIKFAFPLDGGHGIARRVWDYAKVDAIVLVDAVDERPAESKKELDLSLSDLS 120
QY 121 QVPVLVGNKIDIPYASSEDEBLRFTLGLT-MTGGKGVNIGDSNIRPIEVFMCIVAKMG 179
DB 121 TVPELIIGNKIDIPYASSEELRYHGLISNFTTGKGVNIGDSNIRPIEVFMCIVAKMG 180
QY 180 YGSGFKMTTOYI 191
DB 181 YGSGFKMTTOYI 192

RESULT 10
SAR1A BRACM STANDARD; PRT; 193 AA.
ID SAR1A BRACM
AC 004266;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE GTP-binding protein SAR1A.
GN Name=SAR1A;
OS Brassica campestris (field mustard).

CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 CC rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
 CC NCBI_TaxID=3711;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=97298835; PubMed=9154984; DOI=10.1023/A:1005731209124;
 RA Kim W.Y., Cheong N.E., Je D.Y., Kim M.G., Lim C.O., Bahk J.D.,
 RA Cho M.J., Lee S.Y.;
 RT "The presence of a Sar1 gene family in *Brassica campestris* that
 RT suppresses a yeast vesicular transport mutation Sec12-1.";
 RL Plant Mol. Biol. 33:1025-1035(1997).
 CC -1- FUNCTION: Involved in transport from the endoplasmic reticulum to
 CC the Golgi apparatus (By similarity).
 CC -1- TISSUE SPECIFICITY: Expressed in most tissues.
 CC -1- SIMILARITY: Belongs to the small GTPase superfamily. SAR1 family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
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 CC EMBL: U55035; AAC49716.1; -; mRNA.
 DR PIR: T52094; T52094.
 DR HSSP: Q9QVY3; 1F6B.
 DR InterPro: IPR006689; ARF/SAR.
 DR InterPro: IPR001806; Ras_crnsmfng.
 DR InterPro: IPR006687; SAR1_GTP_bd.
 DR InterPro: IPR005225; Small_GTP_bd.
 DR PANTHER: PTHR11711; ARF/SAR; 1.
 DR Pfam: PF00025; Arf; 1.
 DR PRINTS: PR00449; RASTNSFRMG.
 DR PRINTS: PR00328; SAR1GTPBP.
 DR SMART: SM00178; SAR; 1.
 DR TIGRFAMs: TIGR00231; small_GTP; 1.
 DR PROSITE: PS01020; SAR1; 1.
 KM Endoplasmic reticulum: ER-Golgi transport; Golgi stack; GTP-binding;
 KM Nucleotide-binding; Protein transport; Transport.
 FT NP_BIND 27 34 GTP (By similarity).
 FT NP_BIND 70 73 GTP (By similarity).
 FT NP_BIND 129 132 GTP (By similarity).
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 DB 121 TVPFLILGNKIDIPYASSEDELRFTLGLTSGTGGKVDLVGSVNRPLEVFMCSIVRKMG 180
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 DB 181 YGEGFKMNTQYIK 193
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 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Ntsar1 protein.

GN Name=Ntsar1;
 OS Nicotiana tabacum (Common tobacco).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 CC asterids; lamids; Solanales; Solanaceae; Nicotiana.
 CC NCBI_TaxID=4097;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Bright yellow 2;
 RA Takeuchi M., Tada M., Saito C., Yashiroda H., Nakano A.;
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the small GTPase superfamily.
 DR EMBL: D87821; BA013463.1; -; mRNA.
 DR HSSP: Q9QVY3; 1F6B.
 DR GO: GO:0005525; P:intracellular protein transport; IEA.
 DR GO: GO:0006886; P:intracellular protein transport; IEA.
 DR GO: GO:0007264; P:small GTPase mediated signal transduction; IEA.
 DR InterPro: IPR006689; ARF/SAR.
 DR InterPro: IPR001806; Ras_crnsmfng.
 DR InterPro: IPR006687; SAR1_GTP_bd.
 DR InterPro: IPR005225; Small_GTP_bd.
 DR Pfam: PF00025; Arf; 1.
 DR PRINTS: PR00449; RASTNSFRMG.
 DR PRINTS: PR00328; SAR1GTPBP.
 DR SMART: SM00178; SAR; 1.
 DR TIGRFAMs: TIGR00231; small_GTP; 1.
 DR PROSITE: PS01020; SAR1; 1.
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 SQ SEQUENCE 193 AA; 21922 MW; 79F05343EF760A70 CRC64;
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 QY 121 QVPLVLGNKIDIPYASSEDELRFTLGLT-MTTGKGTNLGDSNIRPIEVFMCSIVRKMG 179
 DB 121 TVPFLILGNKIDIPYASSEDELRFTLGLTSGTGGKVDLVGSVNRPLEVFMCSIVRKMG 180
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 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Ras-like small monomeric GTP-binding protein.
 GN Name=SAR1;
 OS Avena fatua (Wild oats).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
 CC Aveneae; Avena.
 CC NCBI_TaxID=4499;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Cranston H.J., Johnson R.R., Chaverra M.E., Dyer W.B.;
 RT "Isolation and characterization of a cDNA encoding a sar1-like
 RT monomeric GTP-binding protein in *Avena fatua* L.";
 RL Plant Sci. 145:75-81(1999).
 CC -1- SIMILARITY: Belongs to the small GTPase superfamily.
 DR EMBL: AF084005; AAC32610.1; -; mRNA.

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Db 121 TVPFLILGNKIDIPYASSDELEFRTGLTGGKGVNLAEISNVPLEVFMCSIVRK 180
Qy 180 -YGEGFKNMTOYIK 192
Db 181 MGYGEGFKMWSQYIK 194

RESULT 15

SARLB BRACM

ID SARLB BRACM STANDARD; PRT; 195 AA.

AC 004267;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE GTP-binding protein SARLB.

GN Name=SARLB;

OS Brassica campestris (field mustard).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

OC rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

OX NCBI_TaxID=3711;

RN [1]

NP NUCLEOTIDE SEQUENCE.

RX MEDLINE=9729835; Pubmed=9154984; DOI=10.1023/A:1005731209124;

RA Kim W.Y., Cheong N.B., Je D.Y., Kim M.G., Lim C.O., Bahk J.D.,

Cho M.J., Lee S.Y.;

RT "The presence of a Sarl gene family in Brassica campestris that

suppresses a yeast vesicular transport mutation Sec12-1.";

RL Plant Mol. Biol. 33:1025-1035(1997).

CC -1- FUNCTION: Involved in transport from the endoplasmic reticulum to

the Golgi apparatus (By similarity).

CC -1- TISSUE SPECIFICITY: Expressed in most tissues.

CC -1- SIMILARITY: Belongs to the small GTPase superfamily. SARL family.

CC -----

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CC use as long as its content is in no way modified and this statement is not

CC removed.

CC -----

CC EMBL: U55036; AAC49717.1; -, mRNA.

DR HSSP; Q9GVY3; 1F6B.

DR InterPro; IPR006689; ARF/SAR.

DR InterPro; IPR001806; Ras trnsfmg.

DR InterPro; IPR006687; SARL_GTP_bd.

DR InterPro; IPR005225; Small_GTP_bd.

DR PANTHER; PTHR11711; ARF/SAR; 1.

DR Pfam; PF00025; Arf; 1.

DR PRINTS; PRO0449; RASTRNSFRNG.

DR PRINTS; PRO0328; SARLGPBP.

DR SMART; SM00178; SAR; 1.

DR TIGRfams; TIGR00231; small_GTP; 1.

DR PROSITE; PS01020; SARL; 1.

KM Endoplasmic reticulum; ER-Golgi transport; Golgi stack; GTP-binding;

KM Nucleotide-binding; Protein transport; Transport.

FT NP_BIND 27 34 GTP (By similarity).

FT NP_BIND 70 73 GTP (By similarity).

FT NP_BIND 129 132 GTP (By similarity).

SQ SEQUENCE 195 AA; 22077 MW; A2FC46B348F29D7B CRC64;

Query March 83.3%; Score 831.5; DB 1; Length 195;

Best Local Similarity 80.9%; Pred. No. 4e-61;

Matches 157; Conservative 19; Mismatches 15; Indels 3; Gaps 2;

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Db 121 TVPFLILGNKIDIPYASSDELEFRTGLTGGKGVNLAEISNVPLEVFMCSIVRK 180
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Job time : 161 secs

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Qy 61 INRVKFAFDLGGHTIARVRWDYAKVDAIVLVDVDRERFAESKEKELDALLSDSILA 120

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 9, 2005, 01:28:26 ; Search time 43 Seconds
(without alignments)
369.157 Million cell updates/sec

Title: US-10-688-481-11

Perfect score: 998

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	998	100.0	192	2	US-09-828-310-11 Sequence 11, Appl
2	614.5	61.6	198	1	US-08-825-780-1 Sequence 1, Appl
3	614.5	61.6	199	2	US-09-149-476-455 Sequence 455, Ap
4	593.5	59.5	193	1	US-08-825-780-4 Sequence 4, Appl
5	585.5	58.7	187	2	US-09-248-796A-20325 Sequence 20325, A
6	575.5	57.7	188	1	US-08-825-780-3 Sequence 3, Appl
7	386	38.7	86	2	US-09-621-976-4318 Sequence 4318, Ap
8	355	35.6	121	2	US-09-621-976-4305 Sequence 4305, Ap
9	277	27.8	181	2	US-09-709-103-53 Sequence 53, Appl
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11	274.5	27.5	186	2	US-09-949-016-9065 Sequence 9065, Ap
12	260	26.1	152	2	US-09-270-767-32983 Sequence 32983, A
13	257.5	25.8	175	2	US-09-103-359-14 Sequence 14, Appl
14	257.5	25.8	179	1	US-08-049-473-32 Sequence 32, Appl
15	257.5	25.8	179	1	US-08-312-648-32 Sequence 32, Appl
16	257.5	25.8	179	4	PCT-US94-04190-32 Sequence 32, Appl
17	246	24.6	170	2	US-09-248-796A-20324 Sequence 20324, A
18	246	24.3	156	2	US-09-621-976-4844 Sequence 4844, Ap
19	242.5	24.3	185	2	US-09-248-796A-20264 Sequence 20264, A
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22	240.5	24.1	181	1	US-08-418-444A-4 Sequence 4, Appl
23	240.5	24.1	181	4	PCT-US94-04190-29 Sequence 29, Appl
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25	239.5	24.0	181	1	US-08-418-444A-7 Sequence 7, Appl
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27	239	23.9	188	2	US-09-270-767-43673 Sequence 43673, A

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29	238.5	23.9	181	1	US-08-049-473-28 Sequence 28, Appl
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32	238.5	23.9	181	1	US-08-418-444A-6 Sequence 6, Appl
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37	236	23.6	181	1	PCT-US94-04190-27 Sequence 27, Appl
38	236	23.6	217	2	US-09-949-016-8523 Sequence 8523, Ap
39	236	23.6	242	2	US-09-949-016-8306 Sequence 8306, Ap
40	236	23.6	262	2	US-09-949-016-8305 Sequence 8305, Ap
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ALIGNMENTS

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RESULT 1
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; Sequence 11, Application US/09828310
; Patent No. 6683938
; GENERAL INFORMATION:
; APPLICANT: COSTA E SILVA, OSWALDO DA
; APPLICANT: BOHNETT, HANS J.
; APPLICANT: VAN THIELEN, NOCHA
; APPLICANT: CHEN, ROUYING
; TITLE OF INVENTION: GTP BINDING STRESS-RELATED PROTEINS AND METHODS OF USE
; FILE REFERENCE: IN PLANTS
; CURRENT APPLICATION NUMBER: US/09/828,310
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/196,001
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1.
; SEQ ID NO 11
; LENGTH: 192
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; ORGANISM: Physcomitrella patens
; US-09-828-310-11

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; Sequence 1, Application US/08825780
; Patent No. 5834238
; GENERAL INFORMATION:
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40	EARLIER FILING DATE: 1997-08-22
41	EARLIER APPLICATION NUMBER: 60/05/7,669
42	EARLIER FILING DATE: 1997-09-05
43	EARLIER APPLICATION NUMBER: 60/04/9,610
44	EARLIER FILING DATE: 1997-06-13
45	EARLIER APPLICATION NUMBER: 60/061,060
46	EARLIER FILING DATE: 1997-10-02

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Query Match      51.6%; Score 614.5; DB 2; Length 199;
Best Local Similarity 59.0%; Pred. No. 1.6e-60;
Matches 115; Conservative 36; Mismatches 39; Indels 5; Gaps 3;

OY      2 FLVDMFY-GF--LASIGLWQKEAKILFLGIDNAGKTTLLHMTKDEKLGCHQHPQYPTSE 57
Db      3 FIFMIMISGSESSVQLQFLGKTKTKLVLFLGIDNAGKTTLLHMTLDBDLGCHVPTLHPTSE 62
OY      58 ELSTNRKFKRFDJGGHTIARVWRDYYAKVDALVYLVDVAVRERFAPSKSEKELSLSDD 117
Db      63 ELTIAGMTFTTFDGLGSHVQARRVKAKYLPAINGLVFLVDCADHRLLESKEKELSLMTDE 122
OY      118 LSLQVPLYVLGNKKIDIPYASSEDELRLFTGL-IWTTGKGVNLGDSNIRPIEFMCSIVR 176
Db      123 TIANVPFLILGNKIDRBPALISEERLREMFGLYQGTGKGSISLKELNARPLEVFMCSVLK 182
OY      177 KKGYGEGEKKMTTOYI 191
Db      183 KQGYEGEGRMAQYI 197

RESULT 4
US-08-825-780-4
; Sequence 4, Application US/08825780
; Patent No. 5834238
; GENERAL INFORMATION:

```

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; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Puri V
; TITLE OF INVENTION: NOVEL HUMAN GTP BINDING P
; TITLE OF INVENTION: ROTENIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/825,780
; FILING DATE: Filed Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0264 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1326351
; US-08-825-780-4

Query Match      59.5%; Score 593.5; DB 1; Length 193;
Best Local Similarity 56.0%; Pred. No. 3.4e-58;
Matches 107; Conservative 38; Mismatches 45; Indels 1; Gaps 1;

QY 2 FLVDFMFGFLASISLGMKEAKITFLGLDNAGKTTLLHMLKDEKLGCHQHOPTSESLSI 61
DB 3 FLWDFGVGLMLGLANRKGKLVFLGLDNAGKTTLLHMLKDRLAQHVPFLHPTSEQMSL 62
QY 62 NRVEKFAFDLGGHTIARRVMDYAKYDAIVYLVDAVDREFAESKKELDLSLSDSLSQ 121
DB 63 GGISFTTYDLGGHQAQRWMDYFPAYDAVFLIDVADAEHMOBSRYELSELDDQGLAS 122
QY 122 VPVILVGNKIDIPYASSEDELRFYGLT-MTTGKGTYNLGDNSIRPIEVFMCSTVRKMGY 180
DB 123 VPVILVGNKIDKPPALSEDQKMQNLINQMCTGKGDVSRNEMASRPMEVFWCSVYLQGY 182
QY 181 GEGFKMTQYI 191
DB 183 GEGIRMLQYI 193

RESULT 5
US-09-248-796A-20325
; Sequence 20325, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
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; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 20325
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Candida albicans
; US-09-248-796A-20325

Query Match      58.7%; Score 585.5; DB 2; Length 187;
Best Local Similarity 63.0%; Pred. No. 2.5e-57;
Matches 114; Conservative 26; Mismatches 40; Indels 1; Gaps 1;

QY 11 LASIGLMOKEAKITFLGLDNAGKTTLLHMLKDEKLGCHQHOPTSESLINRYKFAFD 70
DB 8 LSSDGLNNKAKLFLGLDNAGKTTLLHMLKNDRLATLOFTLHPTSEELIGSVRFTTFD 67
QY 71 LGGHTIARRVMDYAKYDAIVYLVDAVDREFAESKKELDLSLSDSLSQPVLYGNK 130
DB 68 LGCHQAQRRLMKDYFPEVNGIVFLYDAADTERFAESKKELESLEPIELSGVPEVILGNK 127
QY 131 IDIPYASSEDELRFYGLTMTTGKGTYNLGDNSIRPIEVFMCSTVRKMGYGEQFKMTQY 190
DB 128 IDVPTAVGEMELKNALGLYNTTGKDKLPEGT-RPIEVFVSVYMSGYGEAFKWLQY 186
QY 191 I 191
DB 187 I 187

RESULT 6
US-08-825-780-3
; Sequence 3, Application US/08825780
; Patent No. 5834238
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Puri V
; TITLE OF INVENTION: NOVEL HUMAN GTP BINDING P
; TITLE OF INVENTION: ROTENIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/825,780
; FILING DATE: Filed Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0264 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 198 amino acids
; TYPE: amino acid
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/ INFORMATION FOR SEQ ID NO: 32:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 179 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ HYPOTHEICAL: NO
/ ANTI-SENSE: NO
/ FRAGMENT TYPE: N-terminal
/ US-08-312-648-32

Query Match 25.8%; Score 257.5; DB 1; Length 179;

Best Local Similarity 35.6%; Pred. No. 1.1e-20;
Matches 64; Conservative 30; Mismatches 63; Indels 23; Gaps 7;

QY 19 KEAKILFLGLDNAGKTLTLHLKDEKLGQHQPQYPT----SEELSIINRYKFAFDLGGH 74
Db 16 KEMRIIMGLDPAAGKTIILYKL--KLQG-SVTIIPVGFNVETVTKNFKFNWMDVGGQ 71
QY 75 TIARRVRDYYAKVDIVLVDAVDRERFAESKELDSLSDSLSQVPVLGNKIDIP 134
Db 72 DKTRPLMRHYVTGTQGLIFVVDCAHDRIDRDEARQELHRIINDREMDAIIILIFANKQDLR 131
QY 135 YASSEDELRLFTLGLTMTTGKTVNLGDSN--IRPIEVFMCSIVRKMGYSGSGFKMTQYIK 192
Db 132 DAMKPHIEIQEKLG/LT-----RIRDNMWVQP---SCA-TSGDGLYEGLTWLTSTNYK 178

Search completed: December 9, 2005, 01:39:36
Job time : 44 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 9, 2005, 01:32:46 ; Search time 115 Seconds
(without alignments)
697.593 Million cell updates/sec

Title: US-10-688-481-11

Perfect score: 998

Sequence: 1 MFLVDMFYGLASIGLMOKE.....SIVRKMYGEGFKMTQYIK 192

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: Published Applications AA Main:*
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6: /cgn2_6/ptodata/1/pubpaa/us11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	998	100.0	192	3	US-09-828-310-11
2	998	100.0	192	4	US-10-688-481-11
3	880.5	88.2	193	4	US-10-425-115-283016
4	880.5	88.2	193	4	US-10-425-115-283017
5	880.5	88.2	225	4	US-10-425-114-70682
6	880.5	88.2	229	4	US-10-425-114-71236
7	880.5	88.2	236	4	US-10-425-114-61506
8	877.5	87.9	193	4	US-10-767-701-45369
9	872.5	87.4	193	4	US-10-437-963-147565
10	867.5	86.9	255	4	US-10-425-114-64729
11	862.5	86.4	193	4	US-10-424-599-156357
12	862.5	86.4	193	4	US-10-767-701-65953
13	862.5	86.4	193	4	US-10-425-115-128003
14	862.5	86.4	193	4	US-10-425-115-128005
15	862.5	86.4	193	4	US-10-425-115-128006
16	862.5	86.4	208	4	US-10-425-114-51042
17	862.5	86.4	236	4	US-10-425-114-63253
18	862.5	86.4	244	4	US-10-425-114-63253
19	862.5	86.4	251	4	US-10-425-114-50586
20	862.5	86.4	280	4	US-10-425-114-66257
21	859.5	86.1	193	4	US-10-424-599-156355
22	859.5	86.1	266	4	US-10-425-114-45208
23	858.5	86.0	193	4	US-10-425-115-328001
24	856.5	85.8	193	4	US-10-424-599-174038
25	856.5	85.4	193	4	US-10-424-599-182648
26	852.5	85.4	193	4	US-10-437-963-160822
27	843.5	84.5	193	4	US-10-424-599-175209

28	836.5	83.8	191	4	US-10-424-599-175210	Sequence 175210,
29	820.5	82.2	277	4	US-10-437-963-147566	Sequence 147566,
30	789.5	79.1	195	4	US-10-424-599-285372	Sequence 285372,
31	758	76.0	219	4	US-10-437-963-123137	Sequence 123137,
32	744.5	74.6	193	4	US-10-425-115-328658	Sequence 328658,
33	674.5	67.6	193	6	US-11-097-143-15609	Sequence 15609, A
34	665.5	66.7	154	4	US-10-425-115-197017	Sequence 197017,
35	627	62.8	189	4	US-10-128-714-3426	Sequence 3426, Ap
36	615	61.6	189	4	US-10-128-714-8426	Sequence 8426, Ap
37	614.5	61.6	199	3	US-09-809-391-455	Sequence 455, App
38	614.5	61.6	199	3	US-09-882-171-455	Sequence 455, App
39	614.5	61.6	199	4	US-10-164-861-455	Sequence 455, App
40	613.5	61.5	199	4	US-10-032-585-7773	Sequence 7773, Ap
41	612.5	61.4	149	4	US-10-437-963-158424	Sequence 158424,
42	599	60.0	191	4	US-10-320-797-3031	Sequence 3031, Ap
43	593.5	59.5	193	4	US-10-369-493-5976	Sequence 5976, Ap
44	586.5	58.8	198	5	US-10-719-993-472	Sequence 472, App
45	586.5	58.8	198	5	US-10-719-993-473	Sequence 473, App

ALIGNMENTS

```
RESULT 1
US-09-828-310-11
; Sequence 11, Application US/09828310
; Patent No. US20020066124A1
; GENERAL INFORMATION:
; APPLICANT: COSTA E SILVA, OSMALDO DA
; APPLICANT: BOHNETT, HANS J.
; APPLICANT: VAN THIELEN, NOCHA
; APPLICANT: CHEN, ROUYING
; TITLE OF INVENTION: GTP BINDING STRESS-RELATED PROTEINS AND METHODS OF USE
; FILE REFERENCE: 16313-0039
; CURRENT APPLICATION NUMBER: US/09/828,310
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/196,001
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Physcomitrella patens
; US-09-828-310-11

Query Match      100.0%; Score 998; DB 3; Length 192;
Best Local Similarity 100.0%; Pred. No. 4e-99;
Matches 192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MFLVDMFYGLASIGLMOKEAKLFLGLDNAGKTTLLHMLKDKRKGHOPTQYPTSELS 60
Db      1 MFLVDMFYGLASIGLMOKEAKLFLGLDNAGKTTLLHMLKDKRKGHOPTQYPTSELS 60

QY      61 INVKRPAFLGGHTTARVRDYAKVAIVLYLVDAVREPRAESKKEJLSDLSLS 120
Db      61 INVKRPAFLGGHTTARVRDYAKVAIVLYLVDAVREPRAESKKEJLSDLSLS 120

QY      121 QVPLVVGKIKIDIPYASSEDELFITGLITWTGKTGVNLGDSNIRPIEVMCSIVRMGY 180
Db      121 QVPLVVGKIKIDIPYASSEDELFITGLITWTGKTGVNLGDSNIRPIEVMCSIVRMGY 180

QY      181 GEGFKMTQYIK 192
Db      181 GEGFKMTQYIK 192

RESULT 2
US-10-688-481-11
; Sequence 11, Application US/10688481
; Publication No. US20040194163A1
; GENERAL INFORMATION:
```

APPLICANT: COSTA E SILVA, OSWALDO DA
APPLICANT: BOHNET, HANS J.
APPLICANT: VAN THIELEN, NOCHA
APPLICANT: CHEN, ROUYING
TITLE OF INVENTION: GTP BINDING STRESS-RELATED PROTEINS AND METHODS OF USE
TITLE OF INVENTION: IN PLANTS
FILE REFERENCE: 1613-0039
CURRENT APPLICATION NUMBER: US/10/688,481
CURRENT FILING DATE: 2003-10-17
PRIOR APPLICATION NUMBER: 60/196,001
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
LENGTH: 192
TYPE: PRT
ORGANISM: Physcomitrella patens
US-10-688-481-11

Query Match 100.0%; Score 998; DB 4; Length 192;
Best Local Similarity 100.0%; Pred. No. 4e-99;
Matches 192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFLVDMFYGLASIGLMQKEAKILFLGDNAGKTTLLHMLKDEKLGQHPTQYPTSELS 60
DB 1 MFLVDMFYGLASIGLMQKEAKILFLGDNAGKTTLLHMLKDEKLGQHPTQYPTSELS 60
QY 61 INRVKFAFDLGGHTIARRVWRDYAKVDAIVLVDAVDRERPAESKKEIDSLSDSL 120
DB 61 INRVKFAFDLGGHTIARRVWRDYAKVDAIVLVDAVDRERPAESKKEIDSLSDSL 120
QY 121 QVPVLVGNKIDIPYASSEDELRTFLGLTMTGKGVNLDGNSNIRPIEVFMCISVRKMG 180
DB 121 QVPVLVGNKIDIPYASSEDELRTFLGLTMTGKGVNLDGNSNIRPIEVFMCISVRKMG 180
QY 181 GEGFKMTQYIK 192
DB 181 GEGFKMTQYIK 192

RESULT 3

US-10-425-115-283016
Sequence 283016, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 283016
LENGTH: 193
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_21208C.1.pep
US-10-425-115-283016

Query Match 88.2%; Score 880.5; DB 4; Length 193;
Best Local Similarity 84.5%; Pred. No. 2e-86;
Matches 163; Conservative 19; Mismatches 10; Indels 1; Gaps 1;

QY 1 MFLVDMFYGLASIGLMQKEAKILFLGDNAGKTTLLHMLKDEKLGQHPTQYPTSELS 60
DB 1 MFLVDMFYGLASIGLMQKEAKILFLGDNAGKTTLLHMLKDEKLGQHPTQYPTSELS 60
QY 61 INRVKFAFDLGGHTIARRVWRDYAKVDAIVLVDAVDRERPAESKKEIDSLSDSL 120
DB 61 INRVKFAFDLGGHTIARRVWRDYAKVDAIVLVDAVDRERPAESKKEIDSLSDSL 120

DB 61 IGRIFKAFDLGGHQAIRRVWKDYAKVDAIVLVDAVDRERPAESKKEIDALLADSLA 120
QY 121 QVPVLVGNKIDIPYASSEDELRTFLGLT-MTGKGVNLDGNSNIRPIEVFMCISVRKMG 179
DB 121 NVFPLVGNKIDIPYASSEDELRTFLGLT-MTGKGVNLDGNSNIRPIEVFMCISVRKMG 180
QY 180 YGEGFKMTQYIK 192
DB 181 YGEGFKMTQYIK 193

RESULT 4

US-10-425-115-283017
Sequence 283017, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 283017
LENGTH: 193
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_21209C.1.pep
US-10-425-115-283017

Query Match 88.2%; Score 880.5; DB 4; Length 193;
Best Local Similarity 84.5%; Pred. No. 2e-86;
Matches 163; Conservative 19; Mismatches 10; Indels 1; Gaps 1;

QY 1 MFLVDMFYGLASIGLMQKEAKILFLGDNAGKTTLLHMLKDEKLGQHPTQYPTSELS 60
DB 1 MFLVDMFYGLASIGLMQKEAKILFLGDNAGKTTLLHMLKDEKLGQHPTQYPTSELS 60
QY 61 INRVKFAFDLGGHTIARRVWRDYAKVDAIVLVDAVDRERPAESKKEIDSLSDSL 120
DB 61 IGRIFKAFDLGGHQAIRRVWKDYAKVDAIVLVDAVDRERPAESKKEIDALLADSLA 120
QY 121 QVPVLVGNKIDIPYASSEDELRTFLGLT-MTGKGVNLDGNSNIRPIEVFMCISVRKMG 179
DB 121 NVFPLVGNKIDIPYASSEDELRTFLGLT-MTGKGVNLDGNSNIRPIEVFMCISVRKMG 180
QY 180 YGEGFKMTQYIK 192
DB 181 YGEGFKMTQYIK 193

RESULT 5

US-10-425-114-70682
Sequence 70682, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaka, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 70682

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; LENGTH: 225
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3354-056-D12_FLI.pep
; US-10-425-114-70682

Query Match
Best Local Similarity 88.2%; Score 880.5; DB 4; Length 225;
Matches 163; Conservative 19; Mismatches 10; Indels 1; Gaps 1;

Qy 1 MFLVDFYGFPLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGCHOPTQYPTSEELS 60
Db 33 MFLVDFYGFPLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLVQHOPQYPTSEELS 92
Qy 61 INRVKFAFDLGGHTTARRVWDYAKVDAIVYLVDVADERPAESKKEIDSLSDSLS 120
Db 93 IGRIFKFAFDLGGHQAARRVWKDYAKVDAVVYLVDAVDKERPAESKKEIDALLADSLA 152
Qy 121 QVPVLVGNKIDIPYASSEDELRFTLGLT-MTTGKGTVNGDSNIRPIEVFMCISVRKMG 179
Db 153 NVFPLVGNKIDIPYASSEELRYLGLSNFTTGKGVNLADSNVRPLEIFMCSVVRKMG 212
Qy 180 YGEGFKMTOYIK 192
Db 213 YGEGFKMTOYIK 225

RESULT 6
US-10-425-114-71236
; Sequence 71236, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 71236
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-2MFLMO17103E09_FLI.pep
; US-10-425-114-71236

Query Match
Best Local Similarity 88.2%; Score 880.5; DB 4; Length 229;
Matches 163; Conservative 19; Mismatches 10; Indels 1; Gaps 1;

Qy 1 MFLVDFYGFPLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGCHOPTQYPTSEELS 60
Db 37 MFLVDFYGFPLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLVQHOPQYPTSEELS 96
Qy 61 INRVKFAFDLGGHTTARRVWDYAKVDAIVYLVDVADERPAESKKEIDSLSDSLS 120
Db 97 IGRIFKFAFDLGGHQAARRVWKDYAKVDAVVYLVDAVDKERPAESKKEIDALLADSLA 156
Qy 121 QVPVLVGNKIDIPYASSEDELRFTLGLT-MTTGKGTVNGDSNIRPIEVFMCISVRKMG 179
Db 157 NVFPLVGNKIDIPYASSEELRYLGLSNFTTGKGVNLADSNVRPLEIFMCSVVRKMG 216
Qy 180 YGEGFKMTOYIK 192
Db 217 YGEGFKMTOYIK 229
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; LENGTH: 225
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3354-056-D12_FLI.pep
; US-10-425-114-70682

Query Match
Best Local Similarity 88.2%; Score 880.5; DB 4; Length 225;
Matches 163; Conservative 19; Mismatches 10; Indels 1; Gaps 1;

Qy 1 MFLVDFYGFPLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGCHOPTQYPTSEELS 60
Db 33 MFLVDFYGFPLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLVQHOPQYPTSEELS 92
Qy 61 INRVKFAFDLGGHTTARRVWDYAKVDAIVYLVDVADERPAESKKEIDSLSDSLS 120
Db 93 IGRIFKFAFDLGGHQAARRVWKDYAKVDAVVYLVDAVDKERPAESKKEIDALLADSLA 152
Qy 121 QVPVLVGNKIDIPYASSEDELRFTLGLT-MTTGKGTVNGDSNIRPIEVFMCISVRKMG 179
Db 153 NVFPLVGNKIDIPYASSEELRYLGLSNFTTGKGVNLADSNVRPLEIFMCSVVRKMG 212
Qy 180 YGEGFKMTOYIK 192
Db 213 YGEGFKMTOYIK 225

RESULT 6
US-10-425-114-71236
; Sequence 71236, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 71236
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-2MFLMO17103E09_FLI.pep
; US-10-425-114-71236

Query Match
Best Local Similarity 88.2%; Score 880.5; DB 4; Length 229;
Matches 163; Conservative 19; Mismatches 10; Indels 1; Gaps 1;

Qy 1 MFLVDFYGFPLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGCHOPTQYPTSEELS 60
Db 37 MFLVDFYGFPLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLVQHOPQYPTSEELS 96
Qy 61 INRVKFAFDLGGHTTARRVWDYAKVDAIVYLVDVADERPAESKKEIDSLSDSLS 120
Db 97 IGRIFKFAFDLGGHQAARRVWKDYAKVDAVVYLVDAVDKERPAESKKEIDALLADSLA 156
Qy 121 QVPVLVGNKIDIPYASSEDELRFTLGLT-MTTGKGTVNGDSNIRPIEVFMCISVRKMG 179
Db 157 NVFPLVGNKIDIPYASSEELRYLGLSNFTTGKGVNLADSNVRPLEIFMCSVVRKMG 216
Qy 180 YGEGFKMTOYIK 192
Db 217 YGEGFKMTOYIK 229

RESULT 7
US-10-425-114-61506
; Sequence 61506, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 61506
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB143-001-F4_FLI.pep
; US-10-425-114-61506

Query Match
Best Local Similarity 88.2%; Score 880.5; DB 4; Length 236;
Matches 163; Conservative 19; Mismatches 10; Indels 1; Gaps 1;

Qy 1 MFLVDFYGFPLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLGCHOPTQYPTSEELS 60
Db 44 MFLVDFYGFPLASIGLMQKEAKILFLGLDNAGKTTLLHMLKDEKLVQHOPQYPTSEELS 103
Qy 61 INRVKFAFDLGGHTTARRVWDYAKVDAIVYLVDVADERPAESKKEIDSLSDSLS 120
Db 104 IGRIFKFAFDLGGHQAARRVWKDYAKVDAVVYLVDAVDKERPAESKKEIDALLADSLA 163
Qy 121 QVPVLVGNKIDIPYASSEDELRFTLGLT-MTTGKGTVNGDSNIRPIEVFMCISVRKMG 179
Db 164 NVFPLVGNKIDIPYASSEELRYLGLSNFTTGKGVNLADSNVRPLEIFMCSVVRKMG 223
Qy 180 YGEGFKMTOYIK 192
Db 224 YGEGFKMTOYIK 236

RESULT 8
US-10-767-701-45369
; Sequence 45369, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5353)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 45369
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C2820_1.pep
; US-10-767-701-45369

Query Match
Best Local Similarity 87.9%; Score 877.5; DB 4; Length 193;
Matches 163; Conservative 19; Mismatches 10; Indels 1; Gaps 1;
```



```

QY      1 MFLVDMFYGFLASIGLMQKAKILFLGLDNAGKTTLLHMLKDEKLGQHOPQYPTSEELS 60
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 MFLVDMFYGFLASIGLMQKAKILFLGLDNAGKTTLLHMLKDEKLVQHOPQYPTSEELS 60
QY      61 INRVKFAFDLGGHTTARRVWDYAKVDAIVYLVDVDERPFAESKKEIDSLSDSLS 120
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 IGRKFAFDLGGHTTARRVWDYAKVDAIVYLVDVDERPFAESKKEIDSLSDSLSLA 120
QY      121 QVPLVLGNKIDIPYASSEBELRFTLGLT-MTTGKGVNIGDSNIRPIEFVMSIVAKMG 179
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      121 NVPLLLGNKIDIPYASSEBELRYHGLSNFTTOKGKVNIGDSNVRLPLVFMCSVVRKMG 180
QY      180 YGEGFKMNTQYIK 192
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      181 YGEGFKMNSOYIK 193

```

```

RESULT 9
US-10-437-963-147565
; Sequence 147565, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 147565
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURES:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_48081C.1.pep
US-10-437-963-147565

```

```

Query Match      87.4%; Score 872.5; DB 4; Length 193;
Best Local Similarity 83.4%; Pred. No. 1.4e-85;
Matches 161; Conservative 20; Mismatches 11; Indels 1; Gaps 1;

QY      1 MFLVDMFYGFLASIGLMQKAKILFLGLDNAGKTTLLHMLKDEKLGQHOPQYPTSEELS 60
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 MFLVDMFYGFLASIGLMQKAKILFLGLDNAGKTTLLHMLKDEKLVQHOPQYPTSEELS 60
QY      61 INRVKFAFDLGGHTTARRVWDYAKVDAIVYLVDVDERPFAESKKEIDSLSDSLS 120
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 IGRKFAFDLGGHTTARRVWDYAKVDAIVYLVDVDERPFAESKKEIDSLSDSLSLA 120
QY      121 QVPLVLGNKIDIPYASSEBELRFTLGLT-MTTGKGVNIGDSNIRPIEFVMSIVAKMG 179
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      121 TVPLLLGNKIDIPYASSEBELRYHGLSNFTTOKGKVNIGDSNVRLPLVFMCSVVRKMG 180
QY      180 YGEGFKMNTQYIK 192
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      181 YGEGFKMNSOYIK 193

```

```

RESULT 10
US-10-425-114-64729
; Sequence 64729, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingtong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.

```

```

; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 64729
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURES:
; OTHER INFORMATION: Clone ID: LIB4606-001-A8_FLI.pep
US-10-425-114-64729

```

```

Query Match      86.9%; Score 867.5; DB 4; Length 255;
Best Local Similarity 83.4%; Pred. No. 7.3e-85;
Matches 161; Conservative 19; Mismatches 12; Indels 1; Gaps 1;

QY      1 MFLVDMFYGFLASIGLMQKAKILFLGLDNAGKTTLLHMLKDEKLGQHOPQYPTSEELS 60
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      63 MFLVDMFYGFLASIGLMQKAKILFLGLDNAGKTTLLHMLKDEKLVQHOPQYPTSEELS 122
QY      61 INRVKFAFDLGGHTTARRVWDYAKVDAIVYLVDVDERPFAESKKEIDSLSDSLS 120
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      123 IGRKFAFDLGGHTTARRVWDYAKVDAIVYLVDVDERPFAESKKEIDSLSDSLSLA 182
QY      121 QVPLVLGNKIDIPYASSEBELRFTLGLT-MTTGKGVNIGDSNIRPIEFVMSIVAKMG 179
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      183 NVPLLLGNKIDIPYASSEBELRYHGLSNFTTOKGKVNIGDSNVRLPLVFMCSVVRKMG 242
QY      180 YGEGFKMNTQYIK 192
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      243 YGEGFKMNSOYIK 255

```

```

RESULT 11
US-10-424-599-156357
; Sequence 156357, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 156357
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURES:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_112210C.1.pep
US-10-424-599-156357

```

```

Query Match      86.4%; Score 862.5; DB 4; Length 193;
Best Local Similarity 82.9%; Pred. No. 1.7e-84;
Matches 160; Conservative 20; Mismatches 12; Indels 1; Gaps 1;

QY      1 MFLVDMFYGFLASIGLMQKAKILFLGLDNAGKTTLLHMLKDEKLGQHOPQYPTSEELS 60
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 MFLVDMFYGFLASIGLMQKAKILFLGLDNAGKTTLLHMLKDEKLVQHOPQYPTSEELS 60
QY      61 INRVKFAFDLGGHTTARRVWDYAKVDAIVYLVDVDERPFAESKKEIDSLSDSLS 120
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 IGRKFAFDLGGHTTARRVWDYAKVDAIVYLVDVDERPFAESKKEIDSLSDSLSLA 120

```

Qy	Db	Qy	Db
121	QVPLVVLGNKDKIDIPASSSEDELRFTLTGLT-MTTGKGVNLGDSNIRPIPIVFNCSITVRKG	121	QVPLVVLGNKDKIDIPASSSEDELRFTLTGLT-MTTGKGVNLGDSNIRPIPIVFNCSITVRKG
121	TVPFLILGNKDKIDIPASSSEELRHYLTGLTNFTTGKGVNLSDSNVRPMKVFVNCSTVRKG	121	TVPFLILGNKDKIDIPASSSEELRHYLTGLTNFTTGKGVNLSDSNVRPMKVFVNCSTVRKG
180	YGEGRKMTQYIK	192	YGEGRKMTQYIK
181	YGDGFKMLQYIK	193	YGDGFKMLQYIK

```

RESULT 12
US-10-767-701-46953
: Sequence 46953, Application US/10767701
: Publication No. US20040172684A1
: GENERAL INFORMATION:
: APPLICANT: Kovalic, David K.
: APPLICANT: Zhou, Yihua
: APPLICANT: Cao, Yongwei
: TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
: TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
: FILE REFERENCE: 38-21(5353)B
: CURRENT APPLICATION NUMBER: US/10/767,701
: CURRENT FILING DATE: 2004-01-29
: NUMBER OF SEQ ID NOS: 63128
: SEQ ID NO 46953
: LENGTH: 193
: TYPE: PRT
: ORGANISM: Sorghum bicolor
: FEATURE:
: OTHER INFORMATION: Clone ID: SORBI-28MAY03-C49_267.Dep
: US-10-767-701-46953

```

Query Match	86.4%	Score	862.5	DB 4	Length	193			
Best Local Similarity	82.8%	Pred. No.	1.7e-84						
Matches	159	Conservative	22	Mismatches	10	Indels	1	Gaps	1
Qy	1	MLVDMFPGFVLASTGLMCKEAKITLFLGLDNAGKTTLLHMLKDBKQCGQHPTQYPPSSEIS	60						
Db	1	MLVDMFPGVGLASTGLMCKEAKITLFLGLDNAGKTTLLHMLKDBRLVQHPTQYPPSSEIS	60						
Qy	61	INRVKFAKFDLGGHTIARVRMDYYAKVDAYLYLVDAVVRERFAEKKELDSLSDSIS	120						
Db	61	IGKIFKFAFDLGGHGIARVRMKDYAKVDAYLYLVDAVYKKEFAEKKELDALLSDSISLA	120						
Qy	121	QVPVLVLGNKIDIPYASSEDELRFLLGLT-MTTGKTGNLGSNIRPIEVFMCISIVRKKG	179						
Db	121	TVPFLILNKKIDIPYAAASEEELRYHMGLSNFTTGKGNLGSNSVRPLEVFMCISIVRKKG	180						
Qy	180	YGEGFKMTQYI	191						
Db	181	YDGEFKWQSII	192						

```

, RESULT 13
, US-10-425-115-328003
, Sequence 328003, Application US/10425115
, Publication NO. US20040214272A1
, GENERAL INFORMATION:
, APPLICANT: La Rosa, Thomas J.
, APPLICANT: Kovacic, David K.
, APPLICANT: Zhou, Yihua
, APPLICANT: Cao, Yongwei
, TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
, TITLE OF INVENTION: Plants
, FILE REFERENCE: 38-21(53222) B
, CURRENT APPLICATION NUMBER: US/10/425,115
, CURRENT FILING DATE: 2003-04-28
, NUMBER OF SEQ ID NOS: 369326
, SEQ ID NO 328003
, LENGTH: 193
, TYPE: PRT
, ORGANISM: Zea mays
, FEATURE:
, OTHER INFORMATION: Clone ID: MRT4577_62203C.1.pep

```

US-10-425-115-328003	
Query Match	86.4%; Score 862.5; DB 4; Length 193;
Best Local Similarity	82.9%; Pred. No. 1.7e-84;
Matches 160; Conservative	21; Mismatches 11; Indels 1; Gaps 1

Qy	1	MFLVDMFYGGFLAASIGLWQKEAKIIFLGLDNGAKTLLHMLDEKELGQHQPOQYPSSELS	60
Db	1	MFLMDVYGYVLASIGLWQKEAKIIFLGLDNGAKTLLHMLKDEBLVQHQPQHPHSSELS	60
Qy	61	INRYKFAFDLGCHTIIARRVWRDYAKVDAIVLVDAVDRERPAESKKELDLSLSDSL	120
Db	61	IGKIKFPAFDLGCHQIPARRVKDYYAKVDAAVVYLVDAVDKERPAESKKELDALLSDSL	120
Qy	121	QVPLVLVGNKIDIDYYASSEDLRLTLGLT-MTTGKGYNLGDSNIRPILEVPMCSIVRQMG	179
Db	121	NVPLLIIGNKIDIDYYASSEELRYHLGLSNFTTGKGNLGDSDSNVRPLEVPMCSIVRQMG	180
Qy	180	YGEGPKMMTOYIK 192	
Db	181	YGDGPKMVSQYIK 193	

```

RESULT 14
US-10-425-115-328005
; Sequence 328005, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 328005
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_62205C.1.pep
US-10-425-115-328005

```

```

Query Match      86.4%; Score 862.5; DB 4; Length 193;
Best Local Similarity 82.9%; Pred. No. 1.7e-84;
Matches 160; Conservative 21; Mismatches 11; Indels 1; Gaps 1

Qy      1 MFLVDWFGYGLASIGLWQKEAKILFLGIDNAGKTTLLHMLDKEKLGQHQPOTPYTSEELS 60
Db      1 MFLWDWFGYGLASIGLWQKEAKILFLGIDNAGKTTLLHMLDNERLVQHQPONHTPSEELS 60

Qy      61 INRYKFAFDIGGTTIARVRWRDYAKDAIVYLVDADVRRRPAESKKEELSDLSLSDSL 120
Db      61 IGIKIFKFAFDLGGHIIARRVWKDYAKDAVVYLVDAVDKRRPAESKKEELALLSDSLA 120

Qy      121 QVPLVLVGNKIDIPYASSEDELRFTLGLT-WTGGKGTVNLDSNRPPIEVEFMCISIVRKMG 179
Db      121 NVPLILIGNKKIDIPYASSEELRYHLGLSNFTGKGVNLDSNVRFLEVEFMCISVVRKMG 180

Qy      180 YGEGFKMTQYIK 192
Db      181 YGDGFKMVSQYIK 193

RESULT 15
US-10-425-115-328006
; Sequence 328006, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.

```

; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 328006
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_62206C.1.pep
US-10-425-115-328006

Query Match 86.4%; Score 862.5; DB 4; Length 193;

Best Local Similarity 82.9%; Pred. No. 1.7e-84;
Matches 160; Conservative 21; Mismatches 11; Indels 1; Gaps 1;

QY 1 MFLVDMFYGFASIGLWOKBAKILFLGIDNAGKTTLLHMLKDEKLGQHOPTOYPTSEELS 60
DB 1 MFLVDMFYGVLASIGLWOKBAKILFLGIDNAGKTTLLHMLKDEKLVHOPTOYPTSEELS 60
QY 61 INRVKFAFDLGGHTIARRWRDYAKVDAIVLVDAVDRERFAESKKELDSLSDSL 120
DB 61 IGIKFKFAPDLGGHQAIRRVKDYAKVDVAVVLDAYDKERFAESKKELDALSLD 120
QY 121 QVPVLVGNKTDIYASSEDELRFTLGIT-MTTGKTVNLGDSNIRPIEVFMCSIVRMKG 179
DB 121 NVPLILGNKIDIPYASSEELRYHLGINSFTTGKVKNLGDSNVRLPLEVFMCSIVRMKG 180
QY 180 YGEGFKMMTOYIK 192
DB 181 YGEGFKMVSQYIK 193

Search completed: December 9, 2005, 01:41:43
Job time : 117 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: December 9, 2005, 01:35:12 / Search time 25 Seconds
(without alignments)
42.888 Million cell updates/sec

Title: US-10-688-481-11

Perfect score: 998
Sequence: 1 MFLVDMFYGSLASIGLMOKE.....SIVRKMGYGGFKMTQYIK 192

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 32527 seqs, 5584426 residues

Total number of hits satisfying chosen parameters: 32527

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA New:*

- 1: /cgn2_6/ptodaca/1/pubppaa/US06_NEW_PUB pep:*
- 2: /cgn2_6/ptodaca/1/pubppaa/US07_NEW_PUB pep:*
- 3: /cgn2_6/ptodaca/1/pubppaa/US08_NEW_PUB pep:*
- 4: /cgn2_6/ptodaca/1/pubppaa/US09_NEW_PUB pep:*
- 5: /cgn2_6/ptodaca/1/pubppaa/US10_NEW_PUB pep:*
- 6: /cgn2_6/ptodaca/1/pubppaa/US11_NEW_PUB pep:*
- 7: /cgn2_6/ptodaca/1/pubppaa/US12_NEW_PUB pep:*
- 8: /cgn2_6/ptodaca/1/pubppaa/US13_NEW_PUB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	290.5	29.1	179	US-11-093-746A-25	Sequence 25, App1
2	248.5	24.9	242	US-10-821-234-1078	Sequence 1078, App1
3	232	23.2	176	US-11-093-746A-22	Sequence 22, App1
4	224	22.4	173	US-11-093-746A-23	Sequence 23, App1
5	222.5	22.3	201	US-11-093-746A-21	Sequence 21, App1
6	221	22.1	196	US-11-093-746A-2	Sequence 2, App1
7	216.5	21.7	205	US-11-093-746A-26	Sequence 26, App1
8	212.5	21.3	202	US-10-821-234-928	Sequence 928, App1
9	204	20.4	176	US-11-093-746A-24	Sequence 24, App1
10	193.5	19.4	200	US-11-093-746A-19	Sequence 19, App1
11	188.5	18.9	192	US-11-093-746A-20	Sequence 20, App1
12	119.5	12.0	205	US-10-821-234-1454	Sequence 1454, App1
13	118.5	11.9	216	US-10-821-234-1069	Sequence 1069, App1
14	100	10.0	123	US-11-093-691-13	Sequence 13, App1
15	99.5	9.0	408	US-10-821-234-1100	Sequence 1100, App1
16	90	9.0	720	US-10-793-626-2058	Sequence 2058, App1
17	89.5	9.0	448	US-10-618-320A-25	Sequence 25, App1
18	89.5	9.0	458	US-10-618-320A-1	Sequence 1, App1
19	89.5	9.0	458	US-10-821-234-1683	Sequence 1683, App1
20	89	8.9	267	US-11-074-176-322	Sequence 322, App1
21	89	8.9	883	US-11-074-176-88	Sequence 1883, App1
22	89	8.9	883	US-11-074-176-88	Sequence 1883, App1
23	85.5	8.5	394	US-10-821-234-1383	Sequence 1383, App1
24	85	8.5	394	US-10-821-234-1626	Sequence 1626, App1
25	85	8.5	864	US-11-053-100-58	Sequence 58, App1

26	81.5	8.2	301	US-11-074-176-362	Sequence 362, App1
27	81.5	8.2	308	US-11-074-176-254	Sequence 254, App1
28	78.5	7.9	216	US-10-821-234-1483	Sequence 1483, App1
29	78.5	7.9	216	US-10-878-556A-191	Sequence 191, App1
30	76.5	7.7	416	US-10-793-626-1462	Sequence 1462, App1
31	75.5	7.6	353	US-11-060-023-2	Sequence 2, App1
32	75.5	7.6	353	US-11-060-023-6	Sequence 6, App1
33	75.5	7.6	353	US-11-060-023-12	Sequence 12, App1
34	75.5	7.6	353	US-11-060-023-14	Sequence 14, App1
35	75.5	7.6	353	US-11-060-023-15	Sequence 15, App1
36	75.5	7.6	353	US-11-060-023-16	Sequence 16, App1
37	75.5	7.6	353	US-11-060-023-17	Sequence 17, App1
38	75.5	7.6	359	US-11-060-023-11	Sequence 11, App1
39	75.5	7.6	359	US-11-060-023-13	Sequence 13, App1
40	75.5	7.6	360	US-11-060-023-17	Sequence 17, App1
41	75.5	7.6	859	US-11-053-100-52	Sequence 52, App1
42	75.5	7.6	1309	US-11-053-100-53	Sequence 53, App1
43	75.5	7.5	195	US-11-186-284-175	Sequence 175, App1
44	74.5	7.5	374	US-11-060-023-10	Sequence 10, App1
45	74.5	7.5	374	US-11-060-023-10	Sequence 10, App1

ALIGNMENTS

RESULT 1
US-11-093-746A-25
Sequence 25, Application US/11093746A
GENERAL INFORMATION:
APPLICANT: Croce, Carlo M.
TITLE OF INVENTION: NOVEL TUMOR SUPPRESSOR GENE AND
FILE OF INVENTION: COMPOSITIONS AND METHODS FOR MAKING AND USING THE SAME
CURRENT APPLICATION NUMBER: US/11/093,746A
CURRENT FILING DATE: 2005-03-30
PRIOR APPLICATION NUMBER: PCT/US2003/032270
PRIOR FILING DATE: 2003-10-10
PRIOR APPLICATION NUMBER: 60/417,842
PRIOR FILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 25
LENGTH: 179
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-11-093-746A-25

Query Match 29.1%, Score 290.5; DB 7; Length 179;
Best Local Similarity 36.0%, Pred. No. 2.7e-22;
Matches 63; Conservative 29; Mismatches 72; Indels 11; Gaps 1;

18 OKKAKLIFGLDAGKTTLLHMLKDEKLGQHPTQYPTSELSINVKFAPDLGGHTIA 77
15 EKARILLGLDAGKTTLLKQLASEDITVTYTAAPNKKSVADGKLVNVPDGGWKI 74
78 RRVARDYKAVDAIVLVDAVDERPAESKKEIDSLSDSLSQVPVLVGNKIDIPYAS 137
75 RPYKKVYFANTDVLIIVIDCTDRTRLPAGSESEIFEMLMDBRLKQVPLVIFANKQDMDAM 134

138 SEBELAFTGLTMTTQKGVNLDGSMIRPLEVMCSIVKMGVGGGFKMTQYIK 192
135 SAAEVAERKSLVQLGG-----RTWEIRACTRAVDGTGLKEGDVCKKMK 178

RESULT 2
US-10-821-234-1078
Sequence 1078, Application US/10821234
GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit

```

; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821.234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc seq_genes Version 1.0
; SEQ ID NO 1078
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1078

```

```

Query Match          24.9%; Score 248.5; DB 6; Length 242;
Best Local Similarity 32.0%; Pred. No. 6.1e-18;
Matches 62; Conservative 31; Mismatches 78; Indels 23; Gaps 4;

```

```

QY 3 LVDFVYFLASIGLMOKEAKILFLGLDNAGKTTLLHMLKDEKLGQHOPTQYPTSELSI-NRNVKFAFDLGGHTIAR 58
DB 64 LLDWFRSL-----FMKEMELTLVGLQYSGKTTFVNVIAS---QGFSEDMIFTVGFMRK 115
QY 59 LSIIRVYKFAFDLGGHTIARRVWRDYAKVDIYLVDAVDREFFAASKKELSDSLSDS 118
DB 116 VTKGNVVIKIDWIDGOPRFSSMERVCRGVNAIYIMIDADREKIEASRNELHNLDPQ 175
QY 119 LSGVYVVLGNKIDIPYASSEDELFTLGLMTTGKGVNMGDSNINPIEFMCSIYRK 178
DB 176 LOGIPVLVGLGNKRLDPNLDKOL-----IEKNLSAIQDRICISISCKEKD 224
QY 179 GYGEGFKMTQYIK 192
DB 225 NIDITLQMLIQHSK 238

```

```

RESULT 3
US-11-093-746A-22
; Sequence 22, Application US/11093746A
; Publication No. US20050266443A1
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo M.
; APPLICANT: Calin, George A.
; TITLE OF INVENTION: NOVEL TUMOR SUPPRESSOR GENE AND
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MAKING AND USING THE SAME
; FILE REFERENCE: 3589.1015-003
; CURRENT APPLICATION NUMBER: US/11/093,746A
; CURRENT FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: PCT/US2003/032270
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 60/417,842
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-093-746A-22

```

```

Query Match          23.2%; Score 232; DB 7; Length 176;
Best Local Similarity 36.7%; Pred. No. 1.7e-16;
Matches 55; Conservative 25; Mismatches 56; Indels 14; Gaps 2;

```

```

QY 20 EAKLFLGLDNAGKTTLLHMLKDEKLGQHOPTQYPTSELSI-NRNVKFAFDLGGHTIAR 78
DB 12 EAOVVMGLDSAGKTTIYKLGKQNLVDTLPTVGFNVPLPAPGVSLTLMWDIGGQTOLR 71
QY 79 RWMDYVAKVDIYLVDAVDREFFAASKKELSDSLSDSLSQVYVVLGNKIDIPYASS 138
DB 72 ATMKDYLEGIDLVLVLDSTDEARLPEAVALEKVELSDPNMAGVFFVLANKQEPALP 131

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QY 139 EDELRTFLGL-----TMTTGKG 155
DB 132 LLEIRNRLGLBGFQKHCELRACSAITGQG 161

```

```

RESULT 4
US-11-093-746A-23
; Sequence 23, Application US/11093746A
; Publication No. US20050266443A1
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo M.
; APPLICANT: Calin, George A.
; TITLE OF INVENTION: NOVEL TUMOR SUPPRESSOR GENE AND
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MAKING AND USING THE SAME
; FILE REFERENCE: 3589.1015-003
; CURRENT APPLICATION NUMBER: US/11/093,746A
; CURRENT FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: PCT/US2003/032270
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 60/417,842
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-11-093-746A-23

```

```

Query Match          22.4%; Score 224; DB 7; Length 173;
Best Local Similarity 34.6%; Pred. No. 1.1e-15;
Matches 55; Conservative 27; Mismatches 63; Indels 14; Gaps 2;

```

```

QY 11 LASIGLMOKEAKILFLGLDNAGKTTLLHMLKDEKLGQHOPTQYPTSELSI-NRNVKFAF 69
DB 1 MGSVNSRGHAKQVYVNLGLDCAKTTIYKLGKRLVDTLPTVGFNVPLPAPGVSLTLM 60
QY 70 DLGGHTIARRVWRDYAKVDIYLVDAVDREFFAASKKELSDSLSDSLSQVYVVLGN 139
DB 61 DIGGQTOLRATWMDYLEGIDLVLVLDSTDEARLPEAVALEKVELSDPNMAGVFFVLAN 120
QY 130 KIDIPYASSEDELFTLGL-----TMTTGKG 155
DB 121 KQAPDALPLRLIRNRLDLERFODHCWELRACSAITGQG 159

```

```

RESULT 5
US-11-093-746A-21
; Sequence 21, Application US/11093746A
; Publication No. US20050266443A1
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo M.
; APPLICANT: Calin, George A.
; TITLE OF INVENTION: NOVEL TUMOR SUPPRESSOR GENE AND
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MAKING AND USING THE SAME
; FILE REFERENCE: 3589.1015-003
; CURRENT APPLICATION NUMBER: US/11/093,746A
; CURRENT FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: PCT/US2003/032270
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 60/417,842
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-093-746A-21

```

```

Query Match          22.3%; Score 222.5; DB 7; Length 201;
Best Local Similarity 31.7%; Pred. No. 1.6e-15;
Matches 57; Conservative 34; Mismatches 62; Indels 27; Gaps 3;

```

```

Qy 22 IIFELGDNNGKTTLLHMLKDEKLGHOPOVPTSELSI-----NRKYKFAFDLGHTIA 77
Db 24 VVVIIGDSGAKTSLRLKFKFVPSVPTKENTIKIIVPLGSGRGITFPQWMDVGGSEKL 83
Qy 78 RRVWRDYAKVAIVLVDAVDRERFAESKKEJDSLSLDSQVPLVJLGNKRIDIPYAS 137
Db 84 RPLMRSYNRITDGLFVVDPAEAELEEKVELHRIISASDNOGVPALVLANKKDOPGAL 143
Qy 138 SEDELRFTTGL-----TWTTGKGVNLGDSNIRIEVFMCSIRKMGYGEGBFMMTOYI 191
Db 144 SAAEYKRLAVBELAAATITTHVQG-----CSAVDGLGLOQSGLERLIEMI 187

```

```

RESULT 6
US-11-093-746A-2
; Sequence 2, Application US//11093746A
; Publication No. US2005026643A1
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo M.
; APPLICANT: Calin, George A.
; TITLE OF INVENTION: NOVEL TUMOR SUPPRESSOR GENE AND
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MAKING AND USING THE SAME
; FILE REFERENCE: 3589.1015-003
; CURRENT APPLICATION NUMBER: US/11/093,746A
; CURRENT FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: ECT/US2003/032270
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 60/417,842
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 196
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-093-746A-2

```

[illegible]

```

RESULT 7
US-11-093-746A-26
: Sequence 26, Application US/11093746A
: Publication No. US20050266443A1
: GENERAL INFORMATION:
: APPLICANT: Croce, Carlo M.
: APPLICANT: Galin, George A.
: TITLE OF INVENTION: NOVEL TUMOR SUPPRESSOR GENE AND
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MAKING AND USING THE SAME
: FILE REFERENCE: 3589.1015-003
: CURRENT APPLICATION NUMBER: US/11/093,746A
: CURRENT FILING DATE: 2005-03-30
: PRIOR APPLICATION NUMBER: PCT/US2003/032270
: PRIOR FILING DATE: 2003-10-10
: PRIOR APPLICATION NUMBER: 60/417,842
: PRIOR FILING DATE: 2002-10-11
: NUMBER OF SEQ ID NOS: 26
: SOFTWARE: FastSeq for Windows Version 4.0

```

```

; SEO ID NO 26
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-11-093-746A-26

```

Query Match	21.7%	Score 216.5	DB 7	Length 205
Best Local Similarity	29.9%	Pred. No. 7.4e-15		
Matches 52	Conservative 35	Mismatches 76	Indels 11	Gaps 1

Oy . 16 QKEAKILFLGIDNAGKTTLLHMLKDCKLQGHOTQYPRSEELSINRVKFRAFDLGSHTIA 77
 : : ::::: : : : :
Db 15 KSKRIIIMVLGDGSGKTITLYKLGLGVTVPTIGFNLDEVEIKGINFIWMDIGQEKI 74

```
QY      78 RRTWRDYAAKVDAIVLVDAVDRERFAESKKEBLLSDSLSQVPVLVLGNKIDIPYAS 137
       |||:   ::|||: |||: |||: |||: |||: |
DB     75 KRLMRHYFONAGGLIFVVDDSSDSESLSEARNELHRIITLDNELEGACVLVFANKQDSRNAL 134
```

```

Qy      138 SEDELRFLPTGLTMTTGKGTAVNIGDSNIRPIEVFMCSIVRKMGYGGGFFKMTQYI 191
          |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      135 PVAEVANKKLGHSLSKRCWLIG-----TSAISGGQGYEGLEWSTTI 177

```

```

RESULT 8
US-10-821-234-928
; Sequence 928, Application US/10821234
; Publication No. US2005025511A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmant, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for diagnosis and treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 67/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ. ID NOS: 1704
; SOFTWARE: pc_seq_genes Version 1.0
; SEQ ID NO 928
; LENGTH: 202
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-821-234-928

```

	Query Match	21.3%	Score 212.5;	DB 6;	Length 202;
	Best Local Similarity	30.1%;	Pred. No. 1.8e-14;		
	Matches	52;	Conservative	33;	Mismatches 73; Indels 15; Gaps 2
Oy	18 OKEAKILFLGLDNAGKTTLLHMLNDEKLGQHOPYPPTSEELSINRVKFKAPDLGGHTIA	77			
Dd	37 KKQIRILMVGDAAGKTTTLIKLKGELIVTTPITGFNVVEVYKNICFTWMDVGGQORI	96			
Oy	78 RRRRDYYAAKDAILVLYDAVDRERFABSKELDLSLSDSLSSQVPVLVLGNKIDIPAS	137			
Dd	97 RPLMKHFQONTGQIIFVDSNDREIRIQEVDLQKMILLVDELIRAVALLLPANKODLPNAM	156			
Oy	138 SEDLRRLTIGLTMTTGKGVNLGSNSRIPIEVFNCISIVRKMGYG--EGEFKMT	188			
Dd	157 AISMSTDKLG-----QSILNRNTVVOATCATGTGTGYBLDMLS	196			

```

RESULT 9
US-11-093-746A-24
; Sequence 24, Application US/11093746A
; Publication No. US2005026643A1
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo M.
; APPLICANT: Callin, George A.
; TITLE OF INVENTION: NOVEL TUMOR SUPPRESSOR GENE AND
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MAKING AND USING THE SAME
; FILE REFERENCE: 3589.1015-003

```

```

; CURRENT APPLICATION NUMBER: US/11/093,746A
; CURRENT FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: PCT/US2003/032270
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 60/417,842
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Danio rerio
US-11-093-746A-24

Query Match          20.4%; Score 204; DB 7; Length 176;
Best Local Similarity 30.2%; Pred. No. 1.1e-13;
Matches 51; Conservative 32; Mismatches 74; Indels 12; Gaps 2;

QY 17 WQEKALIFLGLDNAGKTTLLHMLKDEKLGQHPTQYPTSEELSI-N-RVKFKAFLDGGHT 75
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 9 FKKPPQVLIWGLDAGSKSTLMYRQLHGVIMQTSPTVGFNVATLQLNKKTSLTWVDIGQD 68
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 76 IARVMDYAKVDAIVYLVDAVDREFAESKKEKLSLSDSLSQVPLVGNKIDIPY 135
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 69 TMRNMRKYIEGCKVLVFDVSDYARIGEQKALKLHDEHLKGVPLVANKDLPN 128
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 136 ASSEDELFTLGLTMTTGKGTNLDGSDNIRPIEFVFCISIVKMGYGEAF 184
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 129 TMTIREYSTKLDLDTYD-----KQWEIQAGSAVKGGLQDAF 166
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
US-11-093-746A-19
; Sequence 19, Application US/11093746A
; Publication No. US20050266443A1
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo M.
; APPLICANT: Calin, George A.
; TITLE OF INVENTION: NOVEL TUMOR SUPPRESSOR GENE AND
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MAKING AND USING THE SAME
; FILE REFERENCE: 3589,1015-003
; CURRENT APPLICATION NUMBER: US/11/093,746A
; CURRENT FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: PCT/US2003/032270
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 60/417,842
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-093-746A-19

Query Match          19.4%; Score 193.5; DB 7; Length 200;
Best Local Similarity 31.6%; Pred. No. 1.4e-12;
Matches 54; Conservative 31; Mismatches 61; Indels 25; Gaps 5;

QY 23 ILFLGLDNAGKTTLLHMLKDEKLGQHPTQYPTSEELSI-----NRVKAFLDGGHTIA 77
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 23 IVIILGLDAGKTTVLYRLQFNEFVNTVPTKGFNTEKIKVTLGNSKTVLFHFWDVGGQEKL 82
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 78 RRVMDYAKVDAIVYLVDAVDREFAESKKEKLSLSDSLSQVPLVGNKIDIPYAS 137
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 83 RPLMKSYSRCTDGIIVFDVSDVVERMEAKTELHKITRISNQGVPVLIANKDLPNSL 142
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 138 SEDELFTLGLTMTTGKGTNLDGSDNIRPIEFVFCISIVKMGYGEAF 185
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 143 SLSELEKLLANG-----ELSSSTPWHLP-----TCALII-----GGGLK 176
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

, RESULT 11
```

```

US-11-093-746A-20
; Sequence 20, Application US/11093746A
; Publication No. US20050266443A1
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo M.
; APPLICANT: Calin, George A.
; TITLE OF INVENTION: NOVEL TUMOR SUPPRESSOR GENE AND
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MAKING AND USING THE SAME
; FILE REFERENCE: 3589,1015-003
; CURRENT APPLICATION NUMBER: US/11/093,746A
; CURRENT FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: PCT/US2003/032270
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 60/417,842
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-093-746A-20

Query Match          18.9%; Score 188.5; DB 7; Length 192;
Best Local Similarity 31.3%; Pred. No. 4.1e-12;
Matches 52; Conservative 30; Mismatches 65; Indels 19; Gaps 4;

QY 23 ILFLGLDNAGKTTLLHMLKDEKLGQHPTQYPTSEELSI-NRVKFA-----FLDGGHTIA 77
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 16 IVMGLDGSACKTIVLYRLKFNENFNTVPTIGFTTEKIKLSNGRAKGISCFHFWGQEKL 75
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 78 RRVMDYAKVDAIVYLVDAVDREFAESKKEKLSLSDSLSQVPLVGNKIDIPYAS 137
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 76 RPLMKSYSRCTDGIIVFDVSDVDRLEAEAKTELHKTKEFENQGTPLVIANKQDLPKSL 135
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 138 SEDELFTLGLTMTTGKGTNLDGSDNIRPIEFVFCISIVKMGYGEAF 183
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 136 PVAIEKQALHLELIPATY-----HVQP-----ACALII-----GEG 167
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
US-10-821-234-1454
; Sequence 1454, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Strache-Crain, Birgit
; APPLICANT: Andarmant, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc seq_genes Version 1.0
; SEQ ID NO 1454
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1454

Query Match          12.0%; Score 119.5; DB 6; Length 205;
Best Local Similarity 25.3%; Pred. No. 3.2e-05;
Matches 48; Conservative 29; Mismatches 60; Indels 53; Gaps 10;

QY 22 KILFLGLDNAGKTTLLHMLKDEKLGQHPTQYPTSEELSI-NRV-----KFAFLDGGHTIA 77
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 13 KLLILIGDSGSGKSCILLRFPDD-----TYESYISTIGVDPKIRITIEDGKTIK 61
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 78 RRVMDYAKVDAIVYLVDAVDREFAESK-----KELDSLSDSLSQV 122
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Db 62 LQIMDAGGERFTTSSYRGAGIIVYDVTDQESFNNVQKMLQELDRYASEN-----V 117
Qy 123 PVLVLGNKID-----IPYASSEDELRLFTLGLTM--TTGKGTYNLGDSDNIRPIEVFM--- 171
Db 118 NKLLVGNKCDLTTKKVVDYTTAK-EPADSLGIFPLETSKATNATVEQ-----FMTMA 169
Qy 172 CSIRKMGYG 181
Db 170 AEIKRMGPG 179

RESULT 13
US-10-821-234-1069
; Sequence 1069, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labac, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmant, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methode for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_genes version 1.0
; SEQ ID NO 1069
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1069

Query Match 11.9%; Score 118.5; DB 6; Length 216;
Best Local Similarity 24.9%; Pred. No. 4,4e-05;
Matches 47; Conservative 28; Mismatches 63; Indels 51; Gaps 9;

Qy 22 KILPFLGIDNAGKTTLLHMLKDEKLGHQPTQYPTSELSINRY----KFAFPLGCHTIA 77
Db 25 KLLIIGDSGVGKSCLLRFADD-----TTYESYSTIGVDPKRTIILDGKTK 73
Qy 78 RRVV-----RDYAKVDAYVLDVADVRERFAESK--KELDSLSDSLSOV 122
Db 74 LQIMDAGGERFTTSSYRGAGIIVYDVTDQESFNNVQKMLQELDRYASEN-----V 129
Qy 123 PVLVLGNKIDIPYASSED-----ELRFTLGLTM--TTGKGTYNLGDSDNIRPIEVFM---C 172
Db 130 NKLLVGNKCDLTTKKVVDYTTAK-EPADSLGIFPLETSKATNATVE-----QAFMTMA 182
Qy 173 SIVRKMGYG 181
Db 183 EIKRMGPG 191

RESULT 14
US-11-099-691-13
; Sequence 13, Application US/11099691
; Publication No. US20050260644A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE PHARMACEUTICALS, INC.
; APPLICANT: BANDMAN, Olga
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: LAL, Preeti
; APPLICANT: YUB, Henry
; APPLICANT: TANG, Y. Tom
; APPLICANT: PATTERSON, Chandra
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: YANG, Junming
; TITLE OF INVENTION: CELL SIGNALING PROTEINS
; FILE REFERENCE: PF-0521 PCT
; CURRENT APPLICATION NUMBER: US/11/099,691
; CURRENT FILING DATE: 2005-04-06

; PRIOR APPLICATION NUMBER: US/09/700,444
; PRIOR FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 60/085,343
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/098,010
; PRIOR FILING DATE: 1998-08-26
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PERL Program
; SEQ ID NO 13
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; OTHER INFORMATION: Incyte Clone 3315936
US-11-099-691-13

Query Match 10.0%; Score 100; DB 7; Length 123;
Best Local Similarity 28.8%; Pred. No. 0.0014;
Matches 23; Conservative 20; Mismatches 35; Indels 2; Gaps 1;

Qy 70 DIGHTIARVWRDYAKVDAYVLDVADVRERFAESKELDSLSDSLSOVPLVLGN 129
Db 5 EIGGSKPFRSYWEMYSKGLLIPVDSADHSRLPEAKTYLHOLIANPV--LPLVEAN 62
Qy 130 KIDIPYASSEDELRLFTLGLT 149
Db 63 KODLEAHYITDIHEALSL 82

RESULT 15
US-10-821-234-1100
; Sequence 1100, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labac, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmant, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methode for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_genes version 1.0
; SEQ ID NO 1100
; LENGTH: 408
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1100

Query Match 10.0%; Score 99.5; DB 6; Length 408;
Best Local Similarity 28.2%; Pred. No. 0.0079;
Matches 31; Conservative 16; Mismatches 38; Indels 25; Gaps 3;

Qy 49 QPTQYPTSELSINRYK-----FKADLGGHTIARVWRDYAKVDAYV 93
Db 218 QSDYIPTQDVLRTKXTGIVETHTFFKDLHFKNPVGSGORSEKRWIHCFCGVTAIIF 277
Qy 94 -----LVDAVDR--RFAESKELDSLSDSLSOVPLVLGNKIDI 133
Db 278 CVALSAVDVLVAEDENRMHESMKLPDSICNNKWFDTJTIILNKKOL 327

Search completed: December 9, 2005, 01:42:19
Job time : 26 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 9, 2005, 01:38:47 | Search time 3390 Seconds

(without alignments)
3219.452 Million cell updates/sec

Title: US-10-688-481-11

Perfect score: 998
Sequence: 1 MFVLVDFYGRGLASIGLMOKE.....SIVRKXMGYGRGPKMTQYIK 192

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Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HAPSI25=500 -MINLEN=40 -MAXLEN=2000000000
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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2: gb_in:.*
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14: gb_hcg:.*
15: gb_pl:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	998	100.0	667	6	AR474309 Sequence
2	998	100.0	667	6	AX282608 Sequence
3	998	100.0	805	6	AR474304 Sequence

C	4	998	100.0	805	6	AX282603
5	876.5	87.8	945	15	AY596178	
6	872.5	87.4	1035	15	AK11979	
7	872.5	87.4	1035	15	AK119548	
8	872.5	87.4	1035	15	AK119548	
9	872.5	87.4	1035	15	AK119548	
10	871.5	87.4	1086	15	AF210431	
11	863.5	86.5	957	15	AF210431	
12	862.5	86.4	613	15	AF210431	
13	862.5	86.4	613	15	AF210431	
14	862.5	86.4	899	15	AF210431	
15	862.5	86.4	899	15	AF210431	
16	862.5	86.4	928	6	AX721083	
17	860.5	86.2	927	15	AK099125	
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19	856.5	85.8	934	15	AK099149	
20	854.5	85.6	966	15	NP35ARGTP	
21	854.5	85.6	1031	15	BT012780	
22	853.5	85.5	613	15	AY117363	
23	853.5	85.5	795	15	AY070378	
24	852.5	85.4	1094	15	AK112012	
25	852.5	85.4	1132	15	AK103351	
26	850.5	85.2	613	15	AY096599	
27	850.5	85.2	904	15	AY085815	
28	850.5	85.2	905	15	ATHGTPB	
29	850.5	85.2	950	15	AY072220	
30	848.5	85.0	857	15	BCU55035	
31	847.5	84.9	1020	15	BCU55035	
32	843.5	84.5	801	15	AF084005	
33	835.5	83.7	709	15	AF048825	
34	832.5	83.4	1013	15	NP50SAR	
35	831.5	83.3	829	15	BCU55036	
36	822.5	82.4	613	15	AY090921	
37	767	76.9	59261	15	AY090921	
38	758	76.0	760	15	AY620416	
39	735.5	73.7	1065	15	NTSAR1	
40	728.5	73.0	994	6	AX461517	
41	728.5	73.0	27502	15	ATAF001535	
42	728.5	73.0	105654	15	ATAF001535	
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44	708.5	71.0	110000	14	CR954214_3	
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ALIGNMENTS

RESULT 1
AR474309 LOCUS AR474309 667 bp DNA
DEFINITION Sequence 6 from patent US 6689939.
ACCESSION AR474309
VERSION AR474309.1 GI:42713157
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 667)
da Costa e Silva, O., Bohner, H.J., van Thiel, N. and Chen, R.
TITLE GTP binding stress-related proteins and methods of use in plants
JOURNAL Patent: US 6689939-A 6 10-FEB-2004;
BASF Plant Science GmbH, Ludwigshafen;
MOX;

FEATURES

source

Location/Qualifiers
1..667
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Alignment Scores:
Pred. No.: 1.14e-96 Length: 667
Score: 998.00 Matches: 192
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-688-481-11 (1-192) x AR474309 (1-667)

Qy 1 MetPheLeuValAspTrrPheTyrGlyPheLeuAlaSerIleGlyLeuTrrGlnLysGlu 20
Db 33 ATGTTTCTTGTAAGTGGTTTACGGCTTCTTCCGAGCAATAGGGCTGTGGCAAGAGAG 92
Qy 21 AlAlaYsIleLeuPheLeuGlyLeuAspAsnAlaGlyLysThrThrLeuLeuHisMetLeu 40
Db 93 GCCAAATCTCTGTTCTGGGCTCGACAAATCTGGCAAGACTACTCTTCTGCAATGCTC 152
Qy 41 LysAspGluLysLeuGlyGlnHisGlnProThrGlnTyrProThrSerGluGluLeuSer 60
Db 153 AAGGATGAGAAATCGGGCAACATCAACCAACGAGATCCAAAGTCAGAGAGAGTTAGT 212
Qy 61 IleAsnArgValLysPheLysAlaPheAspLeuGlyGlyHisThrIleAlaArgVal 80
Db 213 ATCAACAGAGTGAAGTTCAAAGATTCGATCTGGGTGGCCACAAATCGCTCGACGGCTG 272
Qy 81 TrpArgAspTyrTyrAlaLysValAspAlaIleValTyrLeuValAspAlaValAspArg 100
Db 273 TGGAGGACTACTATGCTTAAGGTGATGCTATAGTATCTCGTCGACGAGTAGACAG 332
Qy 101 GluArgPheAlaGluSerLysLysGluLeuAspSerLeuLeuSerAspAspSerLeuSer 120
Db 333 GAGAGATTCTGATGATCAAGAAAGAGCTCGATTCCTCTCCGACGATTCCTGTCC 392
Qy 121 GlnValProValLeuValLeuGlyAsnLysIleAspIleProTyrAlaSerSerGluAsp 140
Db 393 CAAGTTCCTGTGCTCGCTCGTGGAAACAAAGATTAATCCGTCGCTTCTTCTGAAAGAC 452
Qy 141 GluLeuArgPheThrLeuGlyLeuThrMetThrThrGlyLysGlyThrValAsnLeuGly 160
Db 453 GAGTTGGGTTCACTGCTGGTTGACATGACCACTGGTTAAAGAACGGTAAACCTGGGA 512
Qy 161 AspSerAsnIleArgProIleGlnValPheMetCysSerIleValArgLysMetGlyTyr 180
Db 513 GATAGCAACATTCGGCCCATGAGGTTTTCATGTGCAAGTATGTGGCAAAATGGGGTAC 572
Qy 181 GlyGluGlyPheLysTrrPheTrrGlnTyrIleLys 192
Db 573 GGTGAAGGTTTCAAGTGATGACCCAGTACATCAAG 608

RESULT 2
LOCUS AX282608 667 bp DNA linear PAT 02-NOV-2001
DEFINITION Sequence 6 from Patent WO0177161.
ACCESSION AX282608
VERSION AX282608.1 GI:16609685
KEYWORDS
SOURCE Physcomitrella patens
ORGANISM Physcomitrella patens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariaceae; Funariaceae; Physcomitrella.
REFERENCE 1
AUTHORS da Costa e Silva,O., Bohner,H.J., van Thiel,N., and Chen,R.
TITLE GTP binding stress-related proteins and methods of use in plants
JOURNAL Patent: WO 0177161-A 6 18-OCT-2001;
BASF Plant Science GmbH (DE)
FEATURES
source 1..667
location/Qualifiers
/organism="Physcomitrella patens"
/mol_type="unassigned DNA"
/db_xref="taxon:3218"

ORIGIN
Alignment Scores: 1.14e-96 Length: 667
Pred. No.: 998.00 Matches: 192
Score: 998.00
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-688-481-11 (1-192) x AX282608 (1-667)

Qy 1 MetPheLeuValAspTrrPheTyrGlyPheLeuAlaSerIleGlyLeuTrrGlnLysGlu 20
Db 33 ATGTTTCTTGTAAGTGGTTTACGGCTTCTTCCGAGCAATAGGGCTGTGGCAAGAGAG 92
Qy 21 AlAlaYsIleLeuPheLeuGlyLeuAspAsnAlaGlyLysThrThrLeuLeuHisMetLeu 40
Db 93 GCCAAATCTCTGTTCTGGGCTCGACAAATCTGGCAAGACTACTCTTCTGCAATGCTC 152
Qy 41 LysAspGluLysLeuGlyGlnHisGlnProThrGlnTyrProThrSerGluGluLeuSer 60
Db 153 AAGGATGAGAAATCGGGCAACATCAACCAACGAGATCCAAAGTCAGAGAGAGTTAGT 212
Qy 61 IleAsnArgValLysPheLysAlaPheAspLeuGlyGlyHisThrIleAlaArgVal 80
Db 213 ATCAACAGAGTGAAGTTCAAAGATTCGATCTGGGTGGCCACAAATCGCTCGACGGCTG 272
Qy 81 TrpArgAspTyrTyrAlaLysValAspAlaIleValTyrLeuValAspAlaValAspArg 100
Db 273 TGGAGGACTACTATGCTTAAGGTGATGCTATAGTATCTCGTCGACGAGTAGACAG 332
Qy 101 GluArgPheAlaGluSerLysLysGluLeuAspSerLeuLeuSerAspAspSerLeuSer 120
Db 333 GAGAGATTCTGATGATCAAGAAAGAGCTCGATTCCTCTCTCCGACGATTCCTGTCC 392
Qy 121 GlnValProValLeuValLeuGlyAsnLysIleAspIleProTyrAlaSerSerGluAsp 140
Db 393 CAAGTTCCTGTGCTCGCTCGTGGAAACAAAGATTAATCCGTCGCTTCTTCTGAAAGAC 452
Qy 141 GluLeuArgPheThrLeuGlyLeuThrMetThrThrGlyLysGlyThrValAsnLeuGly 160
Db 453 GAGTTGGGTTCACTGCTGGTTGACATGACCACTGGTTAAAGAACGGTAAACCTGGGA 512
Qy 161 AspSerAsnIleArgProIleGlnValPheMetCysSerIleValArgLysMetGlyTyr 180
Db 513 GATAGCAACATTCGGCCCATGAGGTTTTCATGTGCAAGTATGTGGCAAAATGGGGTAC 572
Qy 181 GlyGluGlyPheLysTrrPheTrrGlnTyrIleLys 192
Db 573 GGTGAAGGTTTCAAGTGATGACCCAGTACATCAAG 608

RESULT 3
LOCUS AR474304/c 805 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 1 from patent US 6689339.
ACCESSION AR474304
VERSION AR474304.1 GI:42713152
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 805)
AUTHORS da Costa e Silva,O., Bohner,H.J., van Thiel,N., and Chen,R.
TITLE GTP binding stress-related proteins and methods of use in plants
JOURNAL Patent: US 6689339-A 1 10-FEB-2004;
BASF Plant Science GmbH; Ludwigshafen;
WOX;
FEATURES
source 1..805
location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Alignment Scores: 1.43e-96 Length: 805
Pred. No.: 998.00 Matches: 192
Score: 998.00
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0
US-10-688-481-11 (1-192) x AR474304 (1-805)
QY 1 MetPheLeuValAspTrpPheTyrGlyPheLeuAlaSerIleGlyLeuTTPGlnlyrGlu 20
Db 753 ATGTTCTTGTTGATTGGTTTACGGCTTTCGCGAGCATAGGGCTGTGGCAAGAGAG 694
QY 21 AlaIleIleLeuPheLeuGlyLeuAspAsnAlaGlyIlyrThrThrLeuLeuHismetLeu 40
Db 693 GCCAAATCTGTTTCTGGGCTCGCAATGCTGGCAAGACTACTCTTCTGCAATGCTC 634
QY 41 LysAspGlnLysLeuGlyGlnHisGlnProThrGlnTyrProThrSerGlnGluLeuSer 60
Db 633 AAGGATGAGAACTGGGGCAATCAACCAAGCATTCACACGTTCAGAGAGTTGAGT 574
QY 61 IleAsnArgValIlyrPheLeuValAlaPheAspLeuGlyIlyrThrIleAlaArgArgVal 80
Db 573 ATCAACAGATGAGTCAAGATTCAAGCATTCGATCTGGGCGCACCAATCGCTCGACCGGTG 514
QY 81 TTPArgAspTyrTyrAlaIlyrValAspAlaIleValIlyrLeuValAspAlaValAspArg 100
Db 513 TGGAGGACTACTATGCTAAAGTGGATGCTATGATGATCTCGTCCAGCATGAGACAG 454
QY 101 GluArgPheAlaGlnSerIlyrGlyLeuAspSerLeuSerAspAspSerLeuSer 120
Db 453 GAGAGATTGCTGATGCTAAAGAAAGAGCTGATTTCTTCTCTCCGACGATTCCTGTCC 394
QY 121 GlnValProValIleuValIleuGlyAsnLysIleAspIleProTyrAlaSerSerGluAsp 140
Db 393 CAAGTTCCTGTGCTCGTCTGGGAAACAAGATTGATCCGATCCGCTTCTTCTGAAAGAC 334
QY 141 GluLeuArgPheThrLeuGlyLeuThrMetThrThrGlyIlyrGlyThrValAsnLeuGly 160
Db 333 GAGTTGGGTTTCACTTGGTGGTGAACCATGATCCCTGTAAGAGAAAGGATGGAACCTGGGA 274
QY 161 AspSerAsnIleArgProIleGlnValPheMetCysSerIleValArgLysMetGlyTyr 180
Db 273 GATGCAACATTCCGCCCATTTGAGTTTTCATGTGCGATTTGTGCCCAAAATGGGGTAC 214
QY 181 GlyGlnGlyPheLysTrpMetThrGlnTyrIleLys 192
Db 213 GGTGAAGTTTCAAGTGATGACCAAGTACATCAAG 178
RESULT 4
AX282603/c AX282603 805 bp DNA linear PAT 02-NOV-2001
LOCUS Sequence 1 from Patent WO0177161.
DEFINITION AX282603
ACCESSION AX282603
VERSION AX282603.1 GI:16609680
KEYWORDS
SOURCE
ORGANISM
Phycomitrella patens
Phycomitrella patens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariaceae; Funariales; Funariaceae; Phycomitrella.
REFERENCE
AUTHORS da Costa e Silva, O., Bohner, H.U., van Thiel, N. and Chen, R.
TITLE GTP binding stress-related proteins and methods of use in plants
JOURNAL Patent: WO 0177161-A 1 18-OCT-2001;
BASF Plant Science GmbH (DE)
FEATURES
source location/Qualifiers
1..805
/organism="Phycomitrella patens"
/mol_type="unassigned DNA"
/db_xref="taxon:3218"
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Alignment Scores:
Pred. No.: 1,43e-96 Length: 805
Score: 998.00 Matches: 192
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0
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QY 1 MetPheLeuValAspTrpPheTyrGlyPheLeuAlaSerIleGlyLeuTTPGlnlyrGlu 20
Db 753 ATGTTCTTGTTGATTGGTTTACGGCTTTCGCGAGCATAGGGCTGTGGCAAGAGAG 694
QY 21 AlaIleIleLeuPheLeuGlyLeuAspAsnAlaGlyIlyrThrThrLeuLeuHismetLeu 40
Db 693 GCCAAATCTGTTTCTGGGCTCGCAATGCTGGCAAGACTACTCTTCTGCAATGCTC 634
QY 41 LysAspGlnLysLeuGlyGlnHisGlnProThrGlnTyrProThrSerGlnGluLeuSer 60
Db 633 AAGGATGAGAACTGGGGCAATCAACCAAGCATTCACACGTTCAGAGAGTTGAGT 574
QY 61 IleAsnArgValIlyrPheLeuValAlaPheAspLeuGlyIlyrThrIleAlaArgArgVal 80
Db 573 ATCAACAGATGAGTCAAGATTCAAGCATTCGATCTGGGCGCACCAATCGCTCGACCGGTG 514
QY 81 TTPArgAspTyrTyrAlaIlyrValAspAlaIleValIlyrLeuValAspAlaValAspArg 100
Db 513 TGGAGGACTACTATGCTAAAGTGGATGCTATGATGATCTCGTCCAGCATGAGACAG 454
QY 101 GluArgPheAlaGlnSerIlyrGlyLeuAspSerLeuSerAspAspSerLeuSer 120
Db 453 GAGAGATTGCTGATGCTAAAGAAAGAGCTGATTTCTTCTCTCCGACGATTCCTGTCC 394
QY 121 GlnValProValIleuValIleuGlyAsnLysIleAspIleProTyrAlaSerSerGluAsp 140
Db 393 CAAGTTCCTGTGCTCGTCTGGGAAACAAGATTGATCCGATCCGCTTCTTCTGAAAGAC 334
QY 141 GluLeuArgPheThrLeuGlyLeuThrMetThrThrGlyIlyrGlyThrValAsnLeuGly 160
Db 333 GAGTTGGGTTTCACTTGGTGGTGAACCATGATCCCTGTAAGAGAAAGGATGGAACCTGGGA 274
QY 161 AspSerAsnIleArgProIleGlnValPheMetCysSerIleValArgLysMetGlyTyr 180
Db 273 GATGCAACATTCCGCCCATTTGAGTTTTCATGTGCGATTTGTGCCCAAAATGGGGTAC 214
QY 181 GlyGlnGlyPheLysTrpMetThrGlnTyrIleLys 192
Db 213 GGTGAAGTTTCAAGTGATGACCAAGTACATCAAG 178
RESULT 5
AY596178 945 bp mRNA linear PLN 08-MAY-2004
LOCUS Zea mays putative ras-like small GTP binding protein mRNA, complete
DEFINITION AY596178
ACCESSION AY596178
VERSION AY596178.1 GI:46946655
KEYWORDS
SOURCE
ORGANISM
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
AUTHORS Zhang, Z., Tang, W. and Zheng, Y.
TITLE Suppressing apoptosis is a key mechanism of maize S-CMS restore
JOURNAL Unpublished
2 (bases 1 to 945)
Zhang, Z., Tang, W. and Zheng, Y.
Direct Submission
Submitted (11-APR-2004) National Key Lab of Crop Genetic
Improvement, Huazhong Agricultural University, Wuhan, Hubei
430070, China
FEATURES
source location/Qualifiers
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		PAEKRIPLTLADPSLANVFLIGKRIQDIPYAAASEELRYILGLSNFTTGKQNVLL		
		ADSNVRPLKTIIMCSVVRKMGYGEQFKMSQYIK"		
ORIGIN				
Alignment Scores:				
Pred. No.:	1.46e-83	Length:	945	
Score:	876.50	Matches:	162	
Percent Similarity:	94.30%	Conservative:	20	
Best Local Similarity:	83.94%	Mismatches:	10	
Query Match:	87.83%	Indels:	1	
DB:	15	Gaps:	1	
US-10-688-481-11 (1-192) x AY596178 (1-945)				
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Qy	21	AlAlvylIleLeuPheLeuGlyLeuAlaPheAlaGlyIlyThrThrIleuHisIleLeu	40	
Db	131	GCTAAGATCCCTTCTTCTGGCTCCAGAACCCGGCAGACACCCCTCTTCACATGCTG	190	
Qy	41	LysAspGluIlyIleuGlyGlnHisIleGlnProThrGlnTyrProThrSerGluLeuSer	60	
Db	191	AAGGACGAGCGGCTGTACAGACACCGCAGCGAGTACCCGACGTCAGAGAGTTGAGC	250	
Qy	61	IleAsnArgValIlyPheIlyAlaPheAspLeuGlyGlyHisThrIleAlaArgArgVal	80	
Db	251	ATCGCGAGATCACTAAGTCAAGCGTTCACCTTGGGGCCACAGATGCCCGCGCTC	310	
Qy	81	TrpArgAspTyrTyrAlaIlyValAlaPheAlaIleValTyrLeuValAspAlaValAspArg	100	
Db	311	TGGAAAGACTACTACGCCAAGGTGTATGCTGTGAGTACTGGTGGATGCTTGAACAAG	370	
Qy	101	GluArgPheAlaGlnSerIlyIlyGluLeuAspSerIleuLeuSerAspAspSerLeuSer	120	
Db	371	GAACTTTTGGCGAGTCCAGAAAGAGGCTTGATGCGCTTTCGACGATGACTCCCTTGCA	430	
Qy	121	GlnValProValIleuValIleuGlyAsnIlyIleAspIleProTyrAlaSerSerGluAsp	140	
Db	431	AACGTTCTTCTTCATACTATGGGCAACAAGATGACATCCATACCGGCTTCAAGAGAG	490	
Qy	141	GluLeuArgPheThrIleuGlyLeuThr--MetThrIlyGlyIlyGlyThrValAsnLeu	159	
Db	491	GAGCTGAAGTACTACTCGGCTCGACCAACTTCAACAACCGGGAAGGCAACGTGAACCTTG	550	
Qy	160	GlyAspSerSerAsnIleArgProIleGluValPheMetCysSerIleValIlyGlyPheCly	179	
Db	551	GCCGACTCCAAAGTCCGGCGCTCGAAGATCTTCATGTCAGTGTGTGTGGCAAGATGGCG	610	
Qy	180	TyrGlyGlnGlyPheIlyThrIleThrIlyGlnIlyIlyIly	192	
Db	611	TATGGCGAAGGCTTCAAAATGATGATGCTCAATGATCAACGAG	649	
RESULT 6				
AK111979		1035 bp	mRNA	linear
LOCUS				
DEFINITION				
ACCESSION				
VERSION				
KEYWORDS				
SOURCE				
ORGANISM				

REFERENCE	TITLE
1	The Rice Full-length cDNA Consortium, National Institute of Agricultural Sciences Rice Full-length cDNA Project Team, Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group, Otsu, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kurotsaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Nishikura, J., Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN: Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M., Kigawa, I., Kondo, S., Kono, H., Miyazaki, A., Otsu, N., Ota, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M., and Hayashizaki, Y.
JOURNAL	Collection, mapping, and annotation of over 28,000 cDNA clones from <i>Japonica</i> rice
PUBMED	Science 301 (5631), 376-379 (2003)
REFERENCE	12869764
REFERENCE	TITLE
2	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashidume, W., Hayashizaki, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hirooka, T., Hori, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kigawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kurihara, C., Kurotsaki, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murakami, M., Nagata, T., Nakahama, Y., Nakamura, M., Namiki, T., Narikawa, R., Nishikura, J., Nishii, K., Nomura, K., Numasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H., Otsu, N., Ota, Y., Otsu, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaki-Akahita, S., Tanaka, T., Tomaru, A., Toyota, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S., and Yoshimura, A.
JOURNAL	Rice full-length cDNA
PUBMED	Unpublished
REFERENCE	3 (bases 1 to 1035)
REFERENCE	TITLE
3	Direct Submission Submitted (12-SEP-2002) Shoshi Kikuchi, National Institute of Agricultural Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail: shoshi.kikuchi@affrc.go.jp) Tel: 81-29-858-7007, Fax: 81-29-858-7007
JOURNAL	This clone is one of the 32k full-length cDNA clones from <i>Japonica</i> rice.
COMMENT	URL: http://cdna01.dna.affrc.go.jp/cDNA/NIAS_Rice_Full-length_cDNA_Project_Team_Kikuchi_S_Satoh_K_Nagata_T_Kawagashira_N_Doi_K_Kishimoto_N_Yazaki_J_Ishikawa_M_Yamada_H_Ooka_H_Hotta_I_Kojima_K_Namiki_T_Ohneda_E_Yahagi_W_Suzuki_K_Li_C_Ohtsuki_K_Shishiki_T_Yamamoto_M_and_Nakahama_Y_FAS_Genome_Sequencing_and_Analysis_Group_Otsu_Y_Iida_Y_Fujimura_T_Ikeda_R_Ishibiki_J_Kawamata_M_Kobayashi_M_Kodama_T_Kurotsaki_T_Kusumegi_T_Lu_M_Masuda_H_Miura_J_Mizuno_K_Narikawa_R_Nishikura_J_Oka_M_Ryu_R_Sugano_S_Sugiyama_A_Suzuki_Y_Tsunoda_Y_Ueda_M_Xie_Q_Yokomizo_S_Yoshimura_A_Matsubara_K_and_Murakami_K_Genome_Exploration_Research_Group_in_Riken_Genomic_Sciences_Center_and_Genome_Laboratory_in_Riken Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T.,

Yamamoto, M. and Nakahama, Y.,
 FALS Genome Sequencing & Analysis Group: Otsu, Y., Iida, Y.,
 Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M.,
 Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M.,
 Masuda, H., Miura, J., Mizuno, K., Narikawa, R., Nikura, J., Oka, M.,
 Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tannoda, Y., Ueda, M.,
 Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K. and Murakami, K.,
 Genome Exploration Research Group in Riken Genomic Sciences Center
 and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K.,
 Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T.,
 Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K.,
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 Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J.,
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 Yasunishi, A. and Hayashizaki, Y.

FEATURES

source
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 Location/Qualifiers
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 /mol_type="mRNA"
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ORIGIN

Alignment Scores:
 Pred. No.: 4,34e-83 Length: 1035
 Score: 872.50 Matches: 161
 Percent Similarity: 93.78% Conservative: 20
 Best Local Similarity: 83.42% Mismatch: 11
 Query Match: 87.42% Indels: 1
 DB: 15 Gaps: 1

US-10-688-481-11 (1-192) x AK119548 (1-1035)

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 Oy 21 AAlaValIleLeuPheLeuGlyLeuAspAsnAlaGlyLeuTrpThrLeuLeuH 40
 Db 150 GCCAAGATCTCTTCTCTCGCTCGACCAACGCCGCAAGACCACTCTCACAATGCTC 209
 Oy 41 LysAaPgluLyLeuGlyGlnHieGlnProThrglnTyProThrSerGluGluLeuSer 60
 Db 210 AAGCAGCAGCGGCTCGTCAGACCAAGCGCAGCAGTACCGACGTCGAGAGCTGAGC 269
 Oy 61 IleAsnAaGValLeuPheLeuAlaPheLeuGlyGlnHieGlnProThrIleAlaArgArgVal 80
 Db 270 ATCGCAGAGATCAATTCAAGGCTTCCAGCTCGCGGCGCACAGATGCCCGCGCTC 329
 Oy 81 TrpArgAaPTpTyTyAlaIleValAspAlaIleValTyLeuValAspAlaValAspArg 100
 Db 330 TGGAAAGCATCTACTACGCCAAGCTCATCTGTGTGTTTCTTGCGTGAATGCCGCTGACAA 389
 Oy 101 GluArgPheAlaGluSerIleValSerGluLeuAaPserLeuLeuSerAspAspSerLeuSer 120
 Db 390 GAACGGTTTGGCGAGTCCGAAAGAAAGAACTCGATGCCCTCTTGCGACGATCTCCCTACCA 449
 Oy 121 GlnValProValLeuValLeuGlyAsnIleValIlePheProTyAlaIleSerSerGluAsp 140
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 Oy 141 GluLeuArgPheThrLeuGlyLeuThr---MetTrpThrGlyLeuGlyValThrValAsnLeu 159
 Db 510 GAACCTCCGCTACTACTTGGTGTGAGCAACTTACCAACCGGTAAGGGCAAGCTGAACCTTA 569

Oy 160 GlyAspSerAsnIleAaProlleGluValIlePheMetCysSerIleValArgLysMetGly 179
 Db 570 GCCGACTCCACATCGCGCTCTCGAGATCTTATGTGACGCGCTGTCGCAAGATGGGC 629
 Oy 180 TyGlyGluGlyPheLeuTrpMetTrpGlnTyIleLeu 192
 Db 630 TACGGCAAGCGCTTCAATGATGATGTCCTCATCATCAA 668

RESULT 8
 AK11904
 LOCUS
 DEFINITION
 Oryza sativa (japonica cultivar-group) cDNA clone:J023112F13, full
 insert sequence.
 ACCESSION
 AK11904
 VERSION
 AK11904.1 GI:37988567
 KEYWORDS
 F11 cDNA; CAP trapper.
 SOURCE
 Oryza sativa (japonica cultivar-group)
 ORGANISM
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

1 The Rice Full-length cDNA Consortium, National Institute of
 Agrobiological Sciences Rice Full-length cDNA Project Team,

Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K.,
 Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I.,
 Kojima, K., Nami, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C.,
 Ohtsuki, K., Shishiki, T., Foundation of Advancement of International
 Science Genome Sequencing & Analysis Group: Otsu, Y., Murakami, K.,
 Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tannoda, Y.,
 Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M.,
 Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Nikura, J.,
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 Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Imamura, A., Miura, J.,
 Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S.,
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 Kagawa, I., Kondo, S., Kono, H., Miyazaki, A., Oosato, N., Ota, Y.,
 Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
 Yoshino, M. and Hayashizaki, Y.
 Collection, mapping, and annotation of over 28,000 cDNA clones from
 japonica rice

TITLE

Science 301 (5631), 376-379 (2003)

JOURNLT

12869764

PUBMED

12869764

REFERENCE

12869764

AUTHORS

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K.,
 Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, M.,
 Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hirooka, T.,
 Hori, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K.,
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 Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M.,
 Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M.,
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 Tagami-Takeda, Y., Tagawa, A., Takehashi, F., Takaku-Akahira, S.,
 Tanaka, T., Tomaru, A., Toyota, T., Tannoda, Y., Ueda, M., Waki, K.,
 Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J.,
 Yokomizo, S. and Yoshimura, A.

TITLE

Rice full-length cDNA

JOURNLT

Unpublished

PUBMED

Unpublished

REFERENCE

Unpublished

AUTHORS

Kikuchi, S.
 Direct Submission
 Submitted (12-SEP-2002) Shoshi Kikuchi, National Institute of
 Agrobiological Sciences, Department of Molecular Genetics, Head of
 Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki

Qy 1 MetPheLeuValAspTrpPheTyrglyPheLeuAlaSerIleGlyLeuTrpGlnLeu 20
Db 57 ATGTTCTTGAGTGAAGTCTTCTAGCGGGTGTGGCTCGTGGGGCTGTGGCAAGAAG 116
Qy 21 AlaValIleLeuPheLeuGlyLeuAspAsnAlaGlyIleThrTrpLeuLeuHISMetLeu 40
Db 117 GCCAAGATCCCTTCCTCGGCTCGACAAAGCCGCAAGACACCTCTCCACATGCTC 176
Qy 41 LysAspGlyLeuGlyGlnHISGlnProThrGlnTyrglyProThrSerGlnGluLeuSer 60
Db 177 AAGACCGAGCGGCTCGTGCAGCACCAGCCGACGACGATCCGAGCTCGAGAGACTAGC 236
Qy 61 IleAsnArgValIlePheLeuValPheAspLeuGlyIleThrIleAlaArgVal 80
Db 237 ATCCGCAAGATCAAGTTCAGAGCTCGACCTCGCGCGCCACAGATCGCCGCGCTC 296
Qy 81 TrpArgAspTrpTyrglyAlaValAspAlaIleValTyrglyLeuValAspAlaValAspArg 100
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Db 357 GAACGTTTGGCGAGTGCAGAAAGAACTGATGCCCTCTGCAGACGATTCCTTGCA 416
Qy 121 GlnValProValLeuValLeuGlyAsnIleAspIleProTyrglyAspSerGluAsp 140
Db 417 ACCGTGCTTCTCGATCTGGAACAAAGATCGACATCCCATACGCGCTCGAGAG 476
Qy 141 GluLeuArgPheThrLeuGlyLeuThr---MetThrTrpGlyIleGlyIleValAsnLeu 159
Db 477 GAATCCCGCTACTACTGTGTCTGAGCACTTCACACCGGTAAAGGCAACGTAAACCTA 536
Qy 160 GlyAspSerAsnIleArgProIleGluValPheMetCysSerIleValArgIleMetGly 179
Db 537 GCCACATCCAAAGCGCGGCTCTGAGATCTTCATGTCACAGCTGCTCCGCAATGGGC 596
Qy 180 TyrglyGlnGlyPheLeuTyrglyMetThrGlnTyrglyIleLeu 192
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RESULT 10
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LOCUS Nicotiana tabacum small GTP-binding protein Sar1BNC mRNA, complete cds.
DEFINITION
ACCESSION AF210431 GI:6563321
VERSION AF210431.1
KEYWORDS
SOURCE Nicotiana tabacum (common tobacco)
ORGANISM
REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamiales; Solanales; Solanaceae; Nicotiana.
TITLE 1 (bases 1 to 582)
JOURNAL Andreeva, A.V., Kutzov, M.A., Evans, D.E. and Hawes, C.R.
REFERENCE Plant proteins involved in membrane transport between the endoplasmic reticulum and the Golgi apparatus
AUTHORS Unpublished
TITLE 2 (bases 1 to 582)
JOURNAL Andreeva, A.V.
REFERENCE Direct Submission
TITLE Submitted (02-DEC-1999) Research School of Biological and Molecular Sciences, Oxford Brookes University, Gipsy Lane, Oxford, Oxon OX3 0BP, U.K.
FEATURES
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/db_xref="GI:6563322"
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ORIGIN
Alignment Scores:
Pred. No.: 2,76e-83 Length: 582
Score: 871.50 Matches: 161
Percent Similarity: 94.30% Conservative: 21
Best Local Similarity: 83.42% Mismatches: 10
Query Match: 87.32% Indels: 1
DB: Gaps: 15

US-10-688-481-11 (1-192) x AF210431 (1-582)

Qy 1 MetPheLeuValAspTrpPheTyrglyPheLeuAlaSerIleGlyLeuTrpGlnLeu 20
Db 1 ATGTTCTTGAGTGAAGTCTTCTAGCGGGTGTGGCTCGTGGGGCTGTGGCAAGAAG 60
Qy 21 AlaValIleLeuPheLeuGlyLeuAspAsnAlaGlyIleThrTrpLeuLeuHISMetLeu 40
Db 61 GCTAAGATCTTGTGTTTGGGCTCGATAATCGGCAAAACCACTGTGCTCATATGTTG 120
Qy 41 LysAspGlyLeuGlyGlnHISGlnProThrGlnTyrglyProThrSerGlnGluLeuSer 60
Db 121 AAAGATAGAGATTTGTTCTCAACATCAGCCAAACCAATCCCAAGTTCGAGAGACTT 180
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Db 181 ATTGGCAAGATCAAGTTCAGAGCATTTGATGCTGTCATCAGATTCGCTCGCTGTT 240
Qy 81 TrpArgAspTrpTyrglyAlaValAspAlaIleValTyrglyLeuValAspAlaValAspArg 100
Db 241 TGGAAAGATTAATGCTTAAAGTGAATGCTGTGTATCTTGGAGCTCTTGACAAA 300
Qy 101 GluArgPheAlaGluSerIleGlyLeuAspSerLeuSerAspAspSerLeuSer 120
Db 301 GAAGGTTTCCAGATCCAGAAAGAAAGCTGAGTCTCTCTCTGATGAGTGTGGCC 360
Qy 121 GlnValProValLeuValLeuGlyAsnIleAspIleProTyrglyAspSerGluAsp 140
Db 361 ACTGTTCTTCTCGATCTGGAATCGGTAAACAGATGACATCCCATATGCTGCTCAGAA 420
Qy 141 GluLeuArgPheThrLeuGlyLeuThr---MetThrTrpGlyIleGlyIleValAsnLeu 159
Db 421 GAACGTGTTACCATATGAGGCTTAAAGCGGCTCCACTGCAAGGGAAGTAAACCTG 480
Qy 160 GlyAspSerAsnIleArgProIleGluValPheMetCysSerIleValArgIleMetGly 179
Db 481 GCAGATTCCAATGTCCTCCAGTTGAAGTATTCATGTCAGCATAGTCCCAAAATGGGA 540
Qy 180 TyrglyGlnGlyPheLeuTyrglyMetThrGlnTyrglyIleLeu 192
Db 541 TATGAGAAGGCTTCAAGATGATGTCTCAGTATATCAAG 579

RESULT 11
TOMGTPASE 957 bp mRNA linear PLN 20-APR-1994
LOCUS Lycopersicon esculentum M11. GTPase (SAR2) mRNA, complete cds.
DEFINITION
ACCESSION U12051 L12051
VERSION U12051.1 GI:473683
KEYWORDS
SOURCE Lycopersicon esculentum (Solanum lycopersicum)
ORGANISM
REFERENCE Lycopersicon esculentum
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.
TITLE 1 (bases 1 to 957)
REFERENCE Davies, C.
Cloning and characterization of a tomato GTPase-like gene related

to Yeast and Arabidopsis genes involved in vesicular transport
Plant Mol. Biol. 24 (3), 525-531 (1994)
8123194
PUBMED
COMMENT Original source text: Lycopersicon esculentum (library: lambda
gt11) immature green pericarp cDNA to mRNA.
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118..699
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ORIGIN
Alignment Scores:
Pred. No.: 3,58e-82 Length: 957
Score: 863.50 Matches: 162
Percent Similarity: 92.23% Conservative: 16
Best Local Similarity: 83.94% Mismatches: 14
Query Match: 86.52% Indels: 1
DB: 15 Gaps: 1
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DB 118 ATGTTTCTGGTGGATTGCTTCTAAGAGTGTGGCATCAGGCTTGTGGCAAGAGAT 177
QY 21 AlaValIleLeuPheLeuGlyLeuAspAsnAlaGlyLysThrThrIleLeuLysIleMetLeu 40
DB 178 GCGAAGATCTTGTTTAAAGGCTTGATTAATGCTGGCAAACTACCTTGCTTCATATGTTG 237
QY 41 LysAspGluLysLeuGlyGlnIleGlnProThrGlnTrpProThrSerGluGluLeuSer 60
DB 238 AAGATGAGAGATTGGTGGCAAGCACTACACAGTACCCTCATCAGAGAGTTGAGT 297
QY 61 IleAsnArgValLysPheLysAlaPheAspLeuGlyGlyIleThrIleAlaArgVal 80
DB 298 ATTGGGAATATCAAGTTCAGAGCTTTGATTAGGGGAGACCCAGATTGCTAGAAAGATC 357
QY 81 TrpArgAspTrpTrpTrpAlaLysValAspAlaIleValLysLeuValAspAlaValAspArg 100
DB 358 TGGAGAGACTAATATATGCGAAGTGCAGCTGTTTATCTTGAGACGCAATAGACAGA 417
QY 101 GluArgPheAlaGluSerLysLysGluLeuAspSerLeuLeuSerAspAspSerLeuSer 120
DB 418 GAGAGGTTTCCAGAGCGCAAGAGAAATGGAATGGCGCTTCGTGACAGTACGCTTAAACA 477
QY 121 GlnValProValLeuValLeuGlyAsnLysIleAspIleProTrpAlaSerSerGluAsp 140
DB 478 AATGTCCCATTTTCATTTTGGGAAACAAAGATGATATACATATGCTGCTCAGAAAGAT 537
QY 141 GluLeuArgPheMetLysGlyLeuThr---MetThrArgLysGlyLysValValAsnLeu 159
DB 538 GAGTGGCTTATCACTTGAGCTTACTGCTGACCTGACCAAGGGAACATCAACCTT 597
QY 160 GlyAspSerAsnIleArgProIleGluValPheMetCysSerIleValArgLysMetGly 179
DB 598 GCTGTGACAAATGCGGTCCCAATTGAGGTGTTTATGTGCAGCAATGTCGCGAATAGGGA 657

QY 180 TYGTLGTLGlyPheLysTrpMetTrpGlnTrpIleLys 192
DB 658 TATGTGAGGCTTTCAGTGCATGATGTCGCAATACATCAAG 696
RESULT 12
AY096699
LOCUS
DEFINITION
613 bp mRNA linear PLN 18-SEP-2002
Arabidopsis thaliana putative SAR1/GTP-binding secretory factor
(At4g02080) mRNA, complete cds.
ACCESSION
AY096699.1 GI:20465728
VERSION
KEYWORDS
FLI CDNA.
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE
AUTHORS
Yamada, K., Banb, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M.,
Deng, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L.,
Tang, C.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L.,
Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J.,
Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B.,
Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J.,
Sakurai, T., Satou, M., Seki, M., Shim, P., Southwick, A.,
Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.
Arabidopsis Open Reading Frame (ORF) Clones
2 (bases 1 to 613)
TITILE
JOURNAL
REFERENCE
AUTHORS
Yamada, K., Banb, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M.,
Deng, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L.,
Tang, C.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L.,
Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J.,
Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B.,
Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J.,
Sakurai, T., Satou, M., Seki, M., Shim, P., Southwick, A.,
Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.
Direct Submission
Submitted (16-APR-2002) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
The RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of RAPL cDNAs (RAPL cDNA: 'RIKEN
Arabidopsis Full-length cDNA'): Seki, M., Narusaka, M., Ishida, J.,
Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J.,
Hayashizaki, Y. and Shinozaki, K.
The Salk, Stanford, PGEC (SSP) Consortium members constructed and
sequenced the pUNI (ORF) clones using the RAPL cDNAs: Yamada, K.,
Banb, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M., Deng, J.M.,
Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C.,
Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L., Chen, H.,
Cheuk, R., Jones, T., Karlin-Neumann, G., Kim, C., Lam, B., Lin, J.,
Meyers, M.C., Miranda, M., Nguyen, M., Palm, C.J., Shim, P.,
Southwick, A., Davis, R.W., Ecker, J.R. and Theologis, A.
Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally
to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP
/PGEC) contributed equally to this work as PIs.
Annotation is based on the January 2002 version of the Arabidopsis
genome submitted to GenBank.
FEATURES
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QY 61 ILeaMaRgValIyPheLysAlaPheApeLLeuGlyGlyHisThrIleAlaRgArGVal 80
Db 273 ATGGGAAATCAAGTTTAAGGCTTTGATTGGTGTGTCACAGATTGCTCCGACGGGTC 332
QY 81 TTPArGAspTyrTrAlaLysValaPheAlaIleValTyrLeuValaPheAlaValaPArG 100
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QY 101 GluArGpHeAlaGluSerLysGluLeuApsSerLeuSerApsSerLeuSer 120
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Db 453 AGCGTTCATCTCTCAATTTAGGAAACAGATAGACATACCGTATGCTGCATCAGAGAC 512
QY 141 GluLeuArGpHeThrLeuGlyLeuThr--MetThrThrGlyGlyGlyThrValaenLeu 159
Db 513 GAGCTCCGTTACATCTCGGCTCTCCAACTTCACTACAGAAAGGTAAGGAATCTA 572
QY 160 GluApsSerAenIleArGProIleGluValPheMetCysSerIleValArGlyMetGly 179
Db 573 AGCGATTCCAGATTCAGGATTCAGGATTTTATGTGACGATTCAGGAAATGGGT 632
QY 180 TyrGlyGluGlyPheLysTrpMetThrGlnTyrIleLys 192
Db 633 TACGAGAAAGTTTCAAAATGGGTTTTCATATACATCAAG 671
RESULT 14
ATU56929 899 bp mRNA linear PLN 16-MAY-1996
LOCUS Arabidopsis thaliana GTP binding protein, Sar1 homolog (ASAR1)
DEFINITION mRNA, complete cds.
ACCESSION U56929.1 GI:1314859
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE 1 (bases 1 to 899)
Winge, P., Brembu, T., and Bones, A.M.
The Arabidopsis thaliana Sar-1-like genes belongs to a multigene
family
JOURNAL Unpublished (1996)
REFERENCE 2 (bases 1 to 899)
Winge, P., Brembu, T., and Bones, A.M.
JOURNAL Direct Submission
TITLE Submitted (26-APR-1996) Per Winge, UNIGEN, MTFIS, University of
Trondheim, Olav Kyrresgaat 3, Trondheim N7005, Norway
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Best Local Similarity: 82.90% Mismatches: 11
Query Match: 86.42% Indels: 1
DB: 15 Gaps: 1
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Db 71 ATGTTTCATATCATGATTTGCTTATGCGCTTCGCTTGGGTTATGGCAGAAAG 130
QY 21 AlaLysIleLeuPheLysGlyLeuApsAlaGlyLysThrThrLeuLeuHisMetLeu 40
Db 131 GCTAAGATCTTGTCTCTGGAATCGATTAATGCTGTAAACCACTCTGCTTACATGTTG 190
QY 41 LysaSPGluLysLeuGlyGlnHisGlnProThrGlnTyr-ProThrSerGlnGluLeuSer 60
Db 191 AAAGAGAGAGATGGTATACGATCAGCCATCAGCAGATCCAACTTGTAGAGAACTCAG 250
QY 61 ILeaMaRgValIyPheLysAlaPheApeLLeuGlyGlyHisThrIleAlaRgArGVal 80
Db 251 ATGGGAAATCAAGTTTAAGGCTTTGATTGGTGTGTCACAGATTGCTCCGACGGGTC 310
QY 81 TTPArGAspTyrTrAlaLysValaPheAlaIleValTyrLeuValaPheAlaValaPArG 100
Db 311 TGGAGATTAATCATCTAAGGTGAGCGCTGTCTACCTAGTTAGTTCAGCAAA 370
QY 101 GluArGpHeAlaGluSerLysGluLeuApsSerLeuSerApsSerLeuSer 120
Db 371 GAGAGATTTCAGAAATCAAAAAAGAACTTGAGCACTTCTTCAGACCAATCCCTAGCC 430
QY 121 GlnValProValLeuValLeuGlyAenLysIleApsIleProTyrAlaSerSerGluAps 140
Db 431 AGCGTTCATCTCTCAATTTAGGAAACAGATAGACATACCGTATGCTGCATCAGAGAC 490
QY 141 GluLeuArGpHeThrLeuGlyLeuThr--MetThrThrGlyGlyGlyThrValaenLeu 159
Db 491 GAGCTCCGTTACATCTCGGCTCTCCAACTTCACTACAGAAAGGTAAGGAATCTA 550
QY 160 GluApsSerAenIleArGProIleGluValPheMetCysSerIleValArGlyMetGly 179
Db 551 AGCGATTCCAGATTCAGGATTCAGGATTTTATGTGACGATTCAGGAAATGGGT 610
QY 180 TyrGlyGluGlyPheLysTrpMetThrGlnTyrIleLys 192
Db 611 TACGAGAAAGTTTCAAAATGGGTTTTCATATACATCAAG 649
RESULT 15
AY065357 926 bp mRNA linear PLN 18-SEP-2002
LOCUS Arabidopsis thaliana putative SAR1/GTP-binding secretory factor
DEFINITION (Ac4902080) mRNA, complete cds.
ACCESSION AY065357 GI:17529143
KEYWORDS
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE 1 (bases 1 to 926)
Yamada, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Chung, M.K.,

GenCore version 5.1.6
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OM protein - nucleic search, using frame_p2n model

Run on: December 9, 2005, 01:38:02 ; Search time 469 Seconds
(without alignments)
2728.403 Million cell updates/sec

Title: US-10-688-481-11
Perfect score: 998
Sequence: 1 MFVLDVFGYGLASIGLWQKE.....SIVRKKGYGEGFKMTQYIK 192

Scoring table:
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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4996997 seges, 3332346308 residues
Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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13: geneseqn2004bs:.*
14: geneseqn2005s:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	998	100.0	667	6	ABN89814 Physcomit
2	998	100.0	667	3	ADT91569 Physcomit
3	998	100.0	805	6	ABN89809 Physcomit
4	998	100.0	805	13	ADT91564 Physcomit

5	880.5	88.2	955	13	ADx46899 plant full
6	880.5	88.2	966	13	ADx30716 plant full
7	880.5	88.2	1017	13	ADx62537 plant full
8	871.5	87.3	811	11	ADm45502 insect re
9	871.5	87.3	830	11	ADm45760 insect re
10	867.5	86.9	1164	13	ADx52065 plant full
11	865.5	86.7	615	11	ADm45777 insect re
12	864.5	86.6	1047	13	ADx60523 cotton cd
13	862.5	86.4	876	11	AC134445 rice abio
14	862.5	86.4	885	3	AAc42538 Arabidops
15	862.5	86.4	928	6	ABK71577 Human dit
16	862.5	86.4	966	13	ADx45605 plant full
17	862.5	86.4	998	13	ADx12667 plant full
18	862.5	86.4	1051	13	ADx45551 plant full
19	862.5	86.4	1073	13	ADm81658 plant full
20	862.5	86.4	1117	13	ADx52362 plant full
21	860.5	86.2	952	14	ABE67368 Rice geno
22	859.5	86.1	608	9	AC118989 DNA clone
23	859.5	86.1	928	13	ADx29066 plant full
24	853.5	85.5	807	13	ADx60521 cotton cd
25	852.5	85.4	582	7	ADZ75277 Rice ORF
26	850.5	85.2	904	3	AAc36976 Arabidops
27	848.5	85.0	1233	3	AAc44481 Zea maye
28	842.5	84.4	994	13	ADx60522 cotton cd
29	823.5	82.5	675	6	ABO65802 Arabidops
30	822.5	82.4	582	3	AAc42867 Arabidops
31	820.5	82.2	834	7	ADZ75292 Rice ORF
32	815.5	81.7	592	13	ACN60391 Cotton gy
33	793	79.5	1102	11	AC132345 Rice abio
34	792.5	79.4	640	11	ADm44923 insect re
35	792.5	79.4	669	11	ADm45787 insect re
36	792.5	79.4	669	11	ADm45518 insect re
37	791	79.3	680	11	ADm44921 insect re
38	791	79.3	689	11	ADm45514 insect re
39	791	79.3	689	11	ADm45782 insect re
40	742.5	74.4	657	7	ADZ75275 Rice ORF
41	729.5	73.1	695	9	AC118994 DNA clone
42	728.5	72.7	594	7	ADZ74937 Arabidops
43	725.5	72.7	569	13	ACm48893 cotton pr
44	725.5	72.0	580	11	ADm45500 insect re
45	718.5	72.0	715	11	ADm45798 insect re

ALIGNMENTS

RESULT 1	ABN89814	standard; cDNA; 667 BP.
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AC	ABN89814;	
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DT	18-SEP-2002	(first entry)
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DE	Physcomitrella patens	GBP-1 encoding cDNA sequence SEQ ID NO:6.
XX		
KW	Physcomitrella patens; GBP; GTP binding protein; GBRP; plant;	
KW	GTP binding stress-related protein; transgenic plant; agricultural;	
KW	environmental stress; salinity; drought; temperature; gene; ss.	
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OS	Physcomitrella patens.	
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XX	PN	US2002066124-A1.
XX	PD	30-MAY-2002.
XX		
PF	06-APR-2001;	2001US-00828310.
XX		
PR	07-APR-2000;	2000US-0196001P.

XX (SILV/) SILVA O D C E.
 PA (BOHN/) BOHNERT H J.
 PA (THIE/) THIELEN N V.
 PA (CHEN/) CHEN R.
 XX
 PI Silva ODCE, Bohnert HJ, Thielen NV, Chen R;
 XX
 DR WPI: 2002-556781/59.
 DR P-PSDB: ABB81583.
 XX
 XX Novel GTP binding stress-related proteins and genes encoding the
 PT proteins, useful for producing transgenic plants having increased
 PT tolerance to environmental stress as compared to wild type variety of
 PT plant cell.
 XX
 PS Claim 16; Fig 2A; 73pp; English.
 XX
 XX The present invention describes an isolated GTP binding stress-related
 CC protein (GBSRP) (I) from *Physcomitrella patens*, selected from GTP binding
 CC protein-1 (GBP-1), GBP-2, GBP-3, GBP-4 and GBP-5, or its orthologues. (I)
 CC can be used for producing a transgenic plant (e.g. maize, wheat, rye,
 CC oat, triticale, rice, barley, soybean, peanut, cotton, rapeseed, canola,
 CC manihot, pepper, sunflower, tagetes, solanaceous plants, potato, tobacco,
 CC eggplant, tomato, *Vicia* species, pea, alfalfa, coffee, cacao, tea, *Salix*
 CC species, oil palm, coconut, perennial grass and forage crops). The
 CC transgenic plants produced have increased tolerance to environmental
 CC stress (e.g. salinity, drought and temperature) as compared to a wild
 CC type variety of the plant, from the plant cell. GBSRP polynucleotide
 CC sequences can be used as markers for specific regions of the genome, and
 CC also in functional studies of *P. patens* proteins. They can also be used
 CC for evolutionary and protein structural studies. The present sequence
 CC encodes the *P. patens* GBP-1 protein, which is used in the exemplification
 CC of the present invention
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 SQ Sequence 667 BP, 169 A; 142 C; 185 G; 171 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1.3e-117 Length: 667
 Score: 998.00 Matches: 192
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0
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 QY 1 Methpheuvalaaptrpberryglypheuvalaserllleglyleutrgllyglnu
 Db 33 ATGTTCTTGTAGATTGGTTTACGGCTTTCTTCGAGCATAGGGCTGTGCAGAGAGAG
 QY 21 AAlaystleupheuleuglyleuasphasnalaglylvsthrtrhntleuNH:Metleu 40
 Db 93 GCCAAATCCGTTCGTGGGTGACATGCTGCAGACACTCTTCTGCACATGCTC 152
 QY 41 LysaapglulyleuglyglnH:sglnprrothrglnrtrprothrsersgluldeuser 60
 Db 153 AAGGATGAGAAACGGGGCAATCAACCAACGAGTATCAAGTGCAGAGATTGAGT 212
 QY 61 ILeasnargvallvypheulyalaphespleuglygh:ethrllaalargyval 80
 Db 213 ATCAACAGAGTGAAGTTCAGATTCATCTGGGTGCCACACATGCTCGACGCGTG 272
 QY 81 TTrpargaprryrralalysvalaspralalevalrtrleuvalaspralalasparg 100
 Db 273 TGGAGGAGCTACTAGCTAAGGTGATGCTAAGTATTCGTGACGACGTAGACAGG 332
 QY 101 Gluargpnealaguserlyleuglyleuaspsersleuuseraspsersleuser 120
 Db 333 GAGGATTTGCTGAGTCAAGAGAGAGCTCGATTCTCTCTCGAGCATTTCTGTGCC 392
 QY 121 GlnvalProvalleuvalleuglyasnlyslleaprrleprotyrralaserSerglunsp 140

Db 393 CAAGTTCCTGTGCTGCTCTGGAGAAACAGATTGATATCCGTACGCTTCTTGAAGAC 452
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 Db 453 GAGTTGGCTTACACTTGGTTGACCATGACCATGTAAGAGAACGGTGAACCTGGGA 512
 QY 161 Aspserasnilleargproillegluvalphemetcyaserrllevalarglysmetgly 180
 Db 513 GATAGCAACATTCGGCCCATTTGAGTTTCATGTGCGATTTGTGGCAAAATGGGGTAC 572
 QY 181 Glyluclypheyletrpmetthrnglntyrillelys 192
 Db 573 GGTAAAGTTTCAAGTGAGTACCAGATCATCAAG 608
 RESULT 2
 ID ADT91569 standard; cDNA; 667 BP.
 AC ADT91569;
 XX
 DT 16-DEC-2004 (first entry)
 XX
 DE *Physcomitrella patens* GBP full-length cDNA, PpGBP-1.
 XX
 XX GTP-binding stress-related protein; GBSRP; transgenic plant;
 KM environmental stress tolerance; stress resistance; cell metabolism;
 KM GTP binding protein; GBP; gene; ss.
 XX
 OS *Physcomitrella patens*.
 XX
 FH Key Location/Qualifiers
 FT CDS 33..611
 FT /*tag= a
 FT /product= "PpGBP-1 protein"
 XX
 PN US2004194163-A1.
 XX
 PD 30-SEP-2004.
 XX
 PF 17-OCT-2003; 2003US-00688481.
 XX
 PR 07-APR-2000; 2000US-0196001P.
 PR 06-APR-2001; 2001US-00828310.
 XX
 PA (BADI) BASF PLANT SCI GMBH.
 XX
 PI Da Costa E SilvaO, Bohnert HJ, Thielen NV, Chen R;
 XX
 DR WPI: 2004-698822/68.
 DR P-PSDB: ADT91574.
 XX
 PT Novel isolated nucleic acid encoding polypeptide e.g., GTP-binding stress
 PT related protein, useful for producing vector utilized for producing
 PT transgenic plant that has increased tolerance to environmental stress.
 XX
 PS Claim 12; SEQ ID NO 6; 62pp; English.
 XX
 XX The invention relates to nucleic acid sequences encoding GTP-binding
 CC stress-related proteins (GBSRP). GBSRP DNA is useful for producing a
 CC recombinant expression vector utilized for producing a transgenic plant
 CC that has increased tolerance to environmental stress, for identifying
 CC *Physcomitrella patens* and related organisms, for identifying and
 CC localising *P. patens* sequences of interest, for evolutionary studies, for
 CC determining GBSRP regions required for function, for modulating GBSRP
 CC activity, for modulating metabolism of one or more cell function, for
 CC modulating transport of one or more compounds, for modulating stress
 CC resistance or as markers for specific regions of the genome of *P. patens*.
 CC The present sequence is the *Physcomitrella patens* GTP binding protein
 CC (GBP) full-length cDNA.
 XX
 SQ Sequence 667 BP, 169 A; 142 C; 185 G; 171 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1.3e-117 Length: 667
 Score: 998.00 Matches: 192
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

Pred. No.: 1.3e-117 Length: 667
 Score: 998.00 Matches: 192
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 13 Gaps: 0

US-10-688-481-11 (1-192) x ADR91569 (1-667)

QY 1 MetPheLeuValAspTrpPheTyrGlyPheLeuAlaSerIleGlyLeuTTPGlnlyGlu 20
 DB 33 ATGTTCTTGTAGATTGGTTTACGGCTTCTTGGCGAGATAGGGCTGTGGCAAGAG 92
 QY 21 AlAlaValIleLeuPheLeuGlyLeuAspAsnAlaGlyIleThrThrLeuLeuHISmetLeu 40
 DB 93 GCCAAATCTGTTCTGGGTCTGCAAAAGCTGGCAAGCTACTCTTCTGCAATGCTC 152
 QY 41 LysAspGluLysLeuGlyGlnHISGlnProThrGlnTyrProThrSerGluLeuSer 60
 DB 153 AAGGATGAGAAGCTGGGCAACATCAACCAAGCATATCCAGTCCAGAGAGTTGAGT 212
 QY 61 IleAsnArgValIlePheLeuValaPheAspLeuGlyGlyHISThrIleAlaArgVal 80
 DB 213 ATCAACAGAGTGAAGTCAAGCAATTCGATCTGGTGGCCACCAATCGCTCAACGCTG 272
 QY 81 TrpArgAspTyrTyrAlaLysValaAspAlaIleValTyrLeuValaAspAlaAspArg 100
 DB 273 TGGAGGACTACTACTGCTAAGTGGATGCTATAGTATATCTTCTGCGACGATAGACAG 332
 QY 101 GluArgPheAlaGluSerIlyGlyGluLeuAspSerLeuLeuSerAspAspSerLeuSer 120
 DB 333 GAGGATTTCTGCTGATCAAGAAAGAGCTGATCTCTTCTCTCCGACGATTCCTGTC 392
 QY 121 GlnValProValLeuValLeuGlyAsnLysIleAspIleProTyrAlaSerSerGluAsp 140
 DB 393 CAAGTTCCTGTGCTGCTGCTGGGAAACAGATGATATCCCGTACGCTTCTTGAAGAC 452
 QY 141 GluLeuArgPheThrIleGlyLeuThrMetThrThrGlyGlyGlyThrValaLeuGly 160
 DB 453 GAGTGGGATTCACACTGGGTGACCATGACCACTGGTAAAGACGATGAACCTGGGA 512
 QY 161 AspSerAsnIleArgProIleGluValaPheMetCysSerIleValaArgLysMetGlyTyr 180
 DB 513 GATAGCAACATTCGCGCCCATTTGAGTTTTCATGTGCAGTATTTGGCCAAATGGGGTAC 572
 QY 181 GlyGluGlyPheLysTTPMetThrGlnTyrIleLys 192
 DB 573 GGTAAGTTTCAAGTGATGACCCAGTACATCAAG 608

RESULT 3

ABN89809/c
 ID ABN89809 standard; cDNA; 805 BP.

AC ABN89809;

XX 18-SEP-2002 (first entry)

XX Physcomitrella patens GBP-1 partial cDNA sequence SEQ ID NO:1.

XX Physcomitrella patens; GBP, GTP binding protein; GBSRP, plant;

XX GTP binding stress-related protein; transgenic plant; agricultural;

XX environmental stress; salinity; drought; temperature; gene; ss.

XX Physcomitrella patens.

XX US2002066124-A1.

XX 30-MAY-2002.

XX 06-APR-2001; 2001US-00828310.

XX 07-APR-2000; 2000US-0196001P.

PA (SILV/) SILVA O D C E.
 PA (BOHN/) BOHNERT H J.
 PA (THIE/) THIELEN N V.
 PA (CHEN/) CHEN R.
 PI Silva ODCE, Bohnert HJ, Thielen NV, Chen R;
 XX WPI; 2002-556781/59.

PT Novel GTP binding stress-related proteins and genes encoding the
 PT proteins, useful for producing transgenic plants having increased
 PT tolerance to environmental stress as compared to wild type variety of
 PT plant cell.

PS Example 5; Fig 1A; 73pp; English.

XX The present invention describes an isolated GTP binding stress-related
 CC protein (GBSRP) (1) from Physcomitrella patens, selected from GTP binding
 CC protein-1 (GBP-1), GBP-2, GBP-3, GBP-4 and GBP-5, or its orthologues. (1)
 CC can be used for producing a transgenic plant (e.g. maize, wheat, rye,
 CC oat, triticale, rice, barley, soybean, peanut, cotton, rapeseed, canola,
 CC manioc, pepper, sunflower, legumes, solanaceous plants, potato, tobacco,
 CC eggplant, tomato, Vicia species, pea, alfalfa, coffee, cacao, tea, Salix
 CC species, oil palm, coconut, perennial grass and forage crops). The
 CC transgenic plants produced have increased tolerance to environmental
 CC stress (e.g. salinity, drought and temperature) as compared to a wild
 CC type variety of the plant, from the plant cell. GBSRP polynucleotide
 CC sequences can be used as markers for specific regions of the genome, and
 CC also in functional studies of P. patens proteins. They can also be used
 CC for evolutionary and protein structural studies. The present sequence
 CC represents a P. patens GBP-1 partial cDNA sequence, which is used in the
 CC exemplification of the present invention

XX SQ Sequence 805 BP; 214 A; 218 C; 161 G; 212 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.7e-117 Length: 805
 Score: 998.00 Matches: 192
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-688-481-11 (1-192) x ABN89809 (1-805)

QY 1 MetPheLeuValAspTrpPheTyrGlyPheLeuAlaSerIleGlyLeuTTPGlnlyGlu 20
 DB 753 ATGTTCTTGTAGATTGGTTTACGGCTTCTTGGCGAGATAGGGCTGTGGCAAGAG 694
 QY 21 AlAlaValIleLeuPheLeuGlyLeuAspAsnAlaGlyIleThrThrLeuLeuHISmetLeu 40
 DB 693 GCCAAATCTGTTCTGGGTCTGCAAAAGCTGGCAAGCTACTCTTCTGCAATGCTC 634
 QY 41 LysAspGluLysLeuGlyGlnHISGlnProThrGlnTyrProThrSerGluLeuSer 60
 DB 633 AAGGATGAGAAGCTGGGCAACATCAACCAAGCATATCCAGTCCAGAGAGTTGAGT 574
 QY 61 IleAsnArgValIlePheLeuValaPheAspLeuGlyGlyHISThrIleAlaArgVal 80
 DB 573 ATCAACAGAGTGAAGTCAAGCAATTCGATCTGGTGGCCACCAATCGCTCAACGCTG 514
 QY 81 TrpArgAspTyrTyrAlaLysValaAspAlaIleValTyrLeuValaAspAlaAspArg 100
 DB 513 TGGAGGACTACTACTGCTAAGTGGATGCTATAGTATATCTTCTGCAACGATAGACAG 454
 QY 101 GluArgPheAlaGluSerIlyGlyGluLeuAspSerLeuLeuSerAspAspSerLeuSer 120
 DB 453 GAGAGATTTCTGATGCAAGAAAGAGCTGATTCCTTCTCTCCAGCATTCCTGTC 394
 QY 121 GlnValProValLeuValLeuGlyAsnLysIleAspIleProTyrAlaSerSerGluAsp 140
 DB 393 CAAGTTCCTGCTGCTGCTGCTGGGAAACAGATGATATCCGATGCTTCTTGAAGAC 334

QY 141 GluLeuArgPheThrLeuGlyLeuThrMetThrThrGlyLeuGlyThrValAsnLeuGly 160
Db 333 GAGTTGGCGTTACACTTGGGTTGACCATGACCACTGTAAGGAACGGTGAACCTGGGA 274
QY 161 AspSerAsnIleArgProIleGluValPheMetCysSerIleValArgLeuMetGlyTyr 180
Db 273 GATGACCAACATTCCGCCCATTTGAGGTTTTCATGTGCAGTATTGTGCCAAAATGGGGTAC 214
QY 181 GlyGluGlyPheLeuTyrPheMetThrGlnTyrIleLeu 192
Db 213 GGTGAAGTTTCAAGTGATGATCAACCAAGTACATCAAG 178
RESULT 4
ADT91564/c
ID ADT91564 standard; cDNA; 805 BP.
AC ADT91564;
XX 16-DEC-2004 (first entry)
DT
XX
DE Physcomitrella patens GBSRP EST (expression sequence tag) partial cDNA.
XX
KM GTP-binding stress-related protein; GBSRP; transgenic plant;
KM environmental stress tolerance; stress resistance; cell metabolism; EST;
KM expression sequence tag; ss.
XX
OS Physcomitrella patens.
XX
PN US2004194463-A1.
XX
XX 30-SEP-2004.
PD
XX
PF 17-OCT-2003; 2003US-00688481.
XX
PR 07-APR-2000; 2000US-0196001P.
PR 06-APR-2001; 2001US-00828310.
XX
XX (BAD1) BASF PLANT SCI GMBH.
XX
PI Da Costa E Silveo, Bohner HJ, Thieleen NV, Chen R;
XX
XX WPI; 2004-698822/68.
DR
XX
XX Novel isolated nucleic acid encoding polypeptide e.g., GTP-binding stress
PT -related protein, useful for producing vector utilized for producing
PT transgenic plant that has increased tolerance to environmental stress.
XX
PS Example 5; SEQ ID NO 1; 62pp; English.
XX
XX The invention relates to nucleic acid sequences encoding GTP-binding
CC stress-related protein (GBSRP). GBSRP DNA is useful for producing a
CC recombinant expression vector utilized for producing a transgenic plant
CC that has increased tolerance to environmental stress, for identifying
CC Physcomitrella patens and related organisms, for identifying and
CC localizing P. patens sequences of interest, for evolutionary studies, for
CC determining GBSRP regions required for function, for modulating GBSRP
CC activity, for modulating metabolism of one or more cell function, for
CC modulating transport of one or more compounds, for modulating stress
CC resistance or as markers for specific regions of the genome of P. patens.
CC The present sequence is the Physcomitrella patens GBSRP EST (expression
CC sequence tag) partial cDNA.
XX
XX Sequence 805 BP; 214 A; 218 C; 161 G; 212 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 1.7e-117 Length: 805
Score: 998.00 Matches: 192
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0
US-10-688-481-11 (1-192) x ADT91564 (1-805)

QY 1 MetPheLeuValAspTyrPheTyrGlyPheLeuAlaSerIleGlyLeuTyrGlnLeuGly 20
Db 753 ATGTTCTTGATGATTGGTTTATCGGCTTCTTCCAGAGATAGGGCTGGCGAAGGAG 694
QY 21 AlaIleIleLeuPheLeuGlyLeuAspAsnAlaGlyLeuThrThrLeuLeuHisMetLeu 40
Db 693 GCCAAATCCCTGTTTGTGGGTCGACAAATGCTGGCAAGACTACTCTTCTGCACATGCTC 634
QY 41 LysAspGluLeuLeuGlyGlnHisGlnProThrGlnTyrProThrSerGluGluLeuSer 60
Db 633 AAGCATGAGAACTGGGGCAACATCAACCAACGCAATATCAACGTCAGAGGATTGAGT 574
QY 61 IleAsnArgValIlePheLeuValAspPheLeuGlyGlyHisThrIleAlaArgVal 80
Db 573 ATCAACAGAGTGAAGTCAAAAGCATTCGATCTGGGCGCACCAATCGCTCAACCGG 514
QY 81 TrpArgAspTyrTyrValAlaValAspAlaIleValTyrLeuValAspAlaValAspArg 100
Db 513 TGGAGGACTACTATGCTAAAGTGATGCTATAGTGTATCTCGACGCGATGACAGG 454
QY 101 GluArgPheAlaGluSerIleGlyLeuAspSerLeuLeuSerAspAspSerLeuSer 120
Db 453 GAGGATTTGCTGATGCTCAAGAAAGAAAGCTGATTTCTTCTCCGACGATTTCTGTCC 394
QY 121 GlnValProValIleuValIleuGlyAsnLeuIleAspIleProTyrAlaSerSerGluAsp 140
Db 393 CAAGTTCCTGTGCTCGCTCGGAAACAAGATTGATATCCCTTCCTTCTTGAAGAC 334
QY 141 GluLeuArgPheThrLeuGlyLeuThrMetThrThrGlyLeuGlyThrValAsnLeuGly 160
Db 333 GAGTTGGGTTCCACTTGCTGGTGGACCATGACCACTGGTAAAGAAACGGTGAACCTGGGA 274
QY 161 AspSerAsnIleArgProIleGluValPheMetCysSerIleValArgLeuMetGlyTyr 180
Db 273 GATGACCAACATTCCGCCCATTTGAGGTTTTCATGTGCAGTATTGTGGCAAAATGGGGTAC 214
QY 181 GlyGluGlyPheLeuTyrPheMetThrGlnTyrIleLeu 192
Db 213 GGTGAAGTTTCAAGTGATGATCAACCAAGTACATCAAG 178
RESULT 5
ADX46899
ID ADX46899 standard; cDNA; 955 BP.
XX
XX ADX46899;
AC
XX
DT 21-APR-2005 (first entry)
XX
XX Plant full length insert polynucleotide seqid 21639.
XX
XX plant protectant; plant growth regulant; gene therapy; plant;
KM recombinant DNA construct; physical array; plant breeding marker;
KM cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KM extreme osmotic condition; pathogen tolerance; pest tolerance;
KM growth rate; cell cycle pathway; disease resistance;
KM galactomanan production; lignin production; plant growth regulator;
KM yield; plant growth; plant development; seed oil; protein yield;
KM protein content; gene; ss.
XX
XX unidentified.
XX
XX US2004034888-A1.
XX
XX
XX 19-FEB-2004.
PD
XX
XX 28-APR-2003; 2003US-00425114.
XX
XX 06-MAY-1999; 99US-00304517.
PR
XX 05-NOV-2001; 2001US-00985678.
PR
XX (LITU/) LITU J.
PA (ZHOU/) ZHOU Y.

PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOV/) CAO Y.
XX
PT Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX WPI; 2004-180133/17.
XX
PT New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
PS Claim 1; SEQ ID NO 21639; 15pp; English.
XX
CC The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This sequence represents a plant full length insert
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.
XX
SQ Sequence 955 BP; 219 A; 222 C; 289 G; 225 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 2 32e-102 Length: 955
Score: 880.50 Matches: 163
Percent Similarity: 94.30% Conservative: 19
Best Local Similarity: 84.46% Mismatches: 10
Query Match: 88.23% Indels: 1
DB: 13 Gaps: 1
US-10-688-481-11 (1-192) x ADX46899 (1-955)
QY 1 MetPheLeuValAspTrpPheTyrGlyPheLeuAlaSerIleGlyLeuTrpGlnLeu 20
DB 98 ATGTTCTGTGGTGGTCTGTTCTATGGGGTGTGGCATGCTGGGCTGTGGCAGAAAGAG 157
QY 21 AAlaLysIleLeuPheLeuGlyLeuAspAsnAlaGlyLysThrThrLeuLeuHisMetLeu 40
DB 158 GCTAAGATCTCTTCTCTTGGGCTCGACAACGCCGGAAGAACACCTCTCCACATGCTG 217
QY 41 LysAspGlnLysLeuGlyGlnHisGlnProThrGlnTyrProThrSerGlnGlnLeuSer 60
DB 218 AAGGACGAGCGGCTCGTACAGACACACCAAGAGAACCCACGAGTGAAGAGTTAGC 277
QY 61 IleAsnArgValLysPheLysAlaPheAspLeuGlyGlnHisThrIleAlaArgVal 80
DB 278 ATCGGCAAGATCAAGTTCAGAGCTTGGGGGCCACCGATCGCCCGCGCTC 337
QY 81 TrpArgAspTyrTyrAlaLysValAspAlaIleValTyrLeuValAspAlaValAspArg 100
DB 338 TGGAGAGACTACTACGCGCAAGTTGATGCTGTGTGTAAGTGTGAGATGCTTGAAGA 397
QY 101 GlnArgPheAlaGlnSerLysLysGlnLeuAspSerLeuLeuSerAspAspSerLeuSer 120
DB 398 GAACGTTTTCGCGAGCAAGAGAGAGCTTCATCGCTTTCGAGATGACTCCCTTGCA 457
QY 121 GlnValProValLeuValLeuGlyAsnLysIleAspIleProTyrAlaSerSerGlnAsp 140

DB 458 AACGTTCTTCTCTACTGGGCAACAAGATTGACATCCATCCGCGCTTCAGAGAG 517
QY 141 GlnLeuArgPheThrLeuGlyLeuThr---MetThrThrGlyLysGlyThrValAsnLeu 159
DB 518 GAGCTAGGTAATCACTCTGGGCTGAGACACTTCAACCGGGAAGGCAACGAACTTG 577
QY 160 GlyAspSerAsnIleArgProIleGlnValPheMetCysSerIleValArgLysMetGly 179
DB 578 GCGGACTCCACAGCTCGCCCTCGAGATCTTCATGTGAGTGTGTGGCAAGATGGGC 637
QY 180 TyrGlyGlyGlyPheLysTrpMetThrGlnTyrIleLys 192
DB 638 TATGGCAAGGCTTCAAAATGATGTCTCAGTACATCAAG 676
RESULT 6
ADX30716
ID ADX30716 standard; cDNA; 966 BP.
XX
AC ADX30716;
XX
DT 21-APR-2005 (first entry)
XX
DE Plant full length insert polynucleotide seqid 13536.
XX
XX plant protectant; plant growth regulant; gene therapy; plant;
KM recombinant DNA construct; physical array; plant breeding marker;
KM cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KM extreme osmotic condition; pathogen tolerance; pest tolerance;
KM growth rate; cell cycle pathway; disease resistance;
KM galactomannan production; lignin production; plant growth regulator;
KM yield; plant growth; plant development; seed oil; protein yield;
KM protein content; gene; ss.
XX
OS Unidentified.
XX
PN US2004034888-A1.
XX
PD 19-FEB-2004.
XX
PF 28-APR-2003; 2003US-00425114.
XX
PR 06-MAY-1999; 99US-00304517.
PR 05-NOV-2001; 2001US-00985678.
XX
PA (LIU/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOV/) CAO Y.
XX
PT Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX WPI; 2004-180133/17.
XX
PT New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
PS Claim 1; SEQ ID NO 13536; 15pp; English.
XX
CC The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous

CC recombination in plants, for improving yield by modification of
CC photoynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This sequence represents a plant full length insert
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.

XX
SQ Sequence 966 BP; 225 A; 218 C; 294 G; 229 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2.35e-102 Length: 966
Score: 880.50 Matches: 163
Percent Similarity: 94.30% Conservative: 19
Best Local Similarity: 84.46% Mismatches: 10
Query Match: 88.23% Indels: 1
DB: 13 Gaps: 1

US-10-688-481-11 (1-192) x ADX30716 (1-966)

Qy 1 MetPheLeuValAspTrpPheTyrGlyPheLeuAlaSerIleGlyLeuTrpGlnIlyGlu 20
Db 130 ATGTTCTCGTGGAGCTGCTCTATGCGGGTCTGCGATCGTTGGGCTGTGGCAGAGAG 189
Qy 21 AlAlaValIleLeuPheLeuGlyLeuAspAsnAlaGlyIlyThrTrpLeuLeuHisMetLeu 40
Db 190 GCTAGAGCTCTCTCTGCTGGCTCGACAAAGCCGCGAGACACCCCTCTCCATGCTG 249
Qy 41 LysAspGluIlyLeuGlyGlnIleGlnProThrGlnIlyProThrSerGlyLeuSer 60
Db 250 AAGAGCGAGCGGCTGTCAGACCAAGCCGAGCGAGTACCCAGCTCGAAGAGTTGAGC 309
Qy 61 IleAsnArgValIlyPheLeuAlaPheAspLeuGlyIlyIleThrIleAlaArgArgVal 80
Db 310 ATCGGACAGATCAAGTTCAGAGCGCTTCAGCTTGGGAGCCAGCATGCCCGCGCTC 369
Qy 81 TrpArgAspTrpTyrAlaIlyValAspAlaIleValTyrLeuValAspAlaIlyArg 100
Db 370 TGGAGGAGCTACTACGCGCAAGTTGATCTGTGTGCTTGGGATGCTGTGACAG 429
Qy 101 GluArgPheAlaGluSerIlyLeuGlyLeuAspSerLeuLeuSerAspAspSerLeuSer 120
Db 430 GAACGTTTGGCGAGTCAAGAGAGAGCTTGAATGGCTTCTTTCAGATGACTCCCTTGA 489
Qy 121 GlnValProValIleuValIleuGlyAsnIlyIleAspIleProTyrAlaSerSerGluAsp 140
Db 490 AACGTTCTTCTCTCATCTGGGCAAGATTGATCCATCCATCCGCGCTTCAGAGAG 549
Qy 141 GluLeuArgPheThrIleuGlyIleuThr---MetThrTrpGlyIlyGlyThrValAsnLeu 159
Db 550 GAGCTGAGGAGTACTACTCGGCTGGCAACTTCAACACCGGGAAGGCGCAACGTGAACCTTG 609
Qy 160 GlyAspSerAsnIleArgProIleGlyValPheMetCysSerIleValArgIlyMetCly 179
Db 610 GCCGACTCATGTCGCGGCCCTCGAGAGATCTTCATGTCAGATGAGTGGCGAAGATGGGC 669
Qy 180 TyrGlyGluGlyPheLeuTrpMetThrGlnIlyIleIly 192
Db 670 TATGGCAAGAGCTTCAAAATGATGTCATCATATCAATCAAG 708

RESULT 7
ADX62537
ID ADX62537 standard; cDNA; 1017 BP.
XX
XX ADX62537;
XX
XX 21-APR-2005 (first entry)
XX
XX Plant full length insert polynucleotide seqid 33380.
XX
XX plant prosecretant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;

KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content; gene; ss.
XX
OS Unidentified.
XX
XX US2004034888-A1.
XX
XX 19-FEB-2004.
XX
XX 28-APR-2003; 2003US-00425114.
XX
XX 06-MAY-1999; 99US-00304517.
XX
XX 05-NOV-2001; 2001US-00985678.
XX
XX (Liu/J) LIU J.
XX
XX (ZHOU/J) ZHOU Y.
XX
XX (KOVA/J) KOVALIC D K.
XX
XX (SCRE/J) SCREEN S E.
XX
XX (TAB/J) TABASKA J E.
XX
XX (CAO/J) CAO Y.
XX
XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX
XX WPI; 2004-180133/17.
XX
XX New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
XX Claim 1; SEQ ID NO 33380; 15pp; English.
XX
XX The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.segdata.uspco.gov/sequence.html?DocID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photoynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This sequence represents a plant full length insert
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.

XX
SQ Sequence 1017 BP; 229 A; 229 C; 311 G; 248 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2.53e-102 Length: 1017
Score: 880.50 Matches: 163
Percent Similarity: 94.30% Conservative: 19
Best Local Similarity: 84.46% Mismatches: 10
Query Match: 88.23% Indels: 1
DB: 13 Gaps: 1

US-10-688-481-11 (1-192) x ADX62537 (1-1017)

Qy 1 MetPheLeuValAspTrpPheTyrGlyPheLeuAlaSerIleGlyLeuTrpGlnIlyGlu 20
Db 111 ATGTTCTCGTGGAGCTGCTCTATGCGGGTCTGCGATCGTTGGGCTGTGGCAGAGAG 170
Qy 21 AlAlaValIleLeuPheLeuGlyLeuAspAsnAlaGlyIlyThrTrpLeuLeuHisMetLeu 40
Db 171 GCTAAGATCTCTCTCTGCTGGCTCGACAAAGCCGCGAGACACCCCTCTCCATGCTG 230


```
QY 41 LysAspGluLeuGlyGlnHisGlnProThrGlnTyrProThrSerGluLeuSer 60
D 231 AAGGACGAGCGGCTCGTACAGCACACCGACGAGTACCCGCTAGAAAGTTGAGC 230
QY 61 IleAsnArgValIlePheLeuGlyGlnHisGlnProThrGlnTyrProThrSer 80
D 291 ATCGGCGAGGATCAAGTTCAAGGCGTTCGACCTTGGGGGCCACGATCGCCCGCGTTC 350
QY 81 TrpArgAspTyrTyrIleValIleValIleValTyrLeuValAspAlaValAspArg 100
D 351 TGGAAAGGACTACACGCAAGGTTGATGCTGTGACTTGGGAGTGTGTTGACAAAG 410
QY 101 GluArgPheAlaGluSerLysGluLeuAspSerLeuSerLeuSerLeuSer 120
D 411 GAACGTTTCCGACGTGAAGGAGGAGCTGATCGCTTCTTGACAGTGAATCTCCCTTGC 470
QY 121 GlnValProValIleValIleGlyAsnLysIleAspIleProTyrAlaSerSerGluAsp 140
D 471 AAGCTTCTTCTTCTCATACCTGGGCAACAGATTGACATCCATACGCGGCTTCAGAGAG 530
QY 141 GluLeuArgPheThrLeuGlyLeuThr--MetThrThrGlyLysGlyThrValAsnLeu 159
D 531 GAGCTGAGGTACTACCTCGGCTGAGCACTTCACACCGGAAAGGCAACGTGAACCTTG 590
QY 160 GlyAspSerAsnIleArgProIleGluValPheMetCysSerIleValArgLysMetGly 179
D 591 GCGGACTCCAAATGTCGCGCCCTGAGATCTTCATGTGCACTGTGTCGCAAGATGGGC 650
QY 180 TyrGlyGluGlyPheLeuTyrMetThrGlnTyrIleLys 192
D 651 TATGGCGAAGGCTTCAATGATGATCTCAGTACATCAAG 689
Db
RESULT 8
ADM45502
ID ADM45502 standard; DNA; 811 BP.
AC ADM45502;
XX
DT 03-JUN-2004 (first entry)
DE Insect resistance associated DNA sequence SegID909.
XX
KM Insect resistant phenotype; plant protectant; gene therapy;
KM Arabidopsis thaliana; Nicotiana benthamiana; Oryza sativa;
KM Papaver rhoeas; rice; insect resistance; insect-resistant plant; ds.
XX
OS Unidentified.
XX
PN W02003020025-A2.
XX
PD 13-MAR-2003.
XX
PF 30-AUG-2002; 2002MO-US027882.
XX
PR 31-AUG-2001; 2001US-0316319P.
XX
PA (DOWC ) DOW CHEM CO.
XX
PI Shukla V, Meade T, Lartina I;
XX
DR WPI; 2003-290133/28.
XX
PT New isolated nucleic acid having expression that results in an insect
PT resistant phenotype, useful for conferring insect resistance and for
PT producing insect-resistant plants.
XX
PS Claim 1; SEQ ID NO 909; 396pp; English.
XX
CC This invention relates to a novel isolated nucleic acid comprising, or
CC hybridising under low stringent conditions to, any of the 1214 nucleic
CC acid sequences given in the specification, where the expression of the
CC nucleic acid in a plant results in an insect resistant phenotype. The
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CC invention may be useful as a plant protectant or for gene therapy. The
CC genes are derived from Arabidopsis thaliana, Nicotiana benthamiana, Oryza
CC sativa and Papaver rhoeas. The isolated nucleic acid and vector are
CC useful for conferring insect resistance and for producing insect-
CC resistant plants. The present sequence is that of a DNA sequence of the
CC invention which may confer insect resistance to plants.
XX
SQ Sequence 811 BP; 219 A; 157 C; 199 G; 236 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,61e-101 Length: 811
Score: 871.50 Matches: 161
Percent Similarity: 94.30% Conservative: 21
Best Local Similarity: 83.42% Mismatches: 10
Query Match: 87.32% Indels: 1
DB: 11 Gaps: 1

US-10-688-481-11 (1-192) x ADM45502 (1-811)
QY 1 MetPheLeuValAspTrpPheTyrGlyPheLeuAlaSerIleGlyLeuTrpGlnLysGlu 20
D 131 ATGTTCTTGGTACATTGGTTCTATGGAATTCAGCAACCTCGGATTATGCGAAGAG 190
QY 21 AlaLysIleLeuPheLeuGlyLeuAspAsnAlaGlyLysThrThrLeuLeuHisMetLeu 40
D 191 GCTAAGATCTTGTGTTTGGGCTCGATTAATGCCGCAAAACCACTTACTCATATGTTG 250
QY 41 LysAspGluLeuGlyGlnHisGlnProThrGlnTyrProThrSerGluLeuSer 60
D 251 AAAGATGAAGATGGTTCACATTCAGCCCAACATATCCGACGTCAGAGGAGCTTAGT 310
QY 61 IleAsnArgValIlePheLeuValIlePheAspLeuGlyGlnHisGlnProThrGlnTyrProThrSer 80
D 311 ATCGGCAAGTCAAGTTCAAAGCATTGACTTGGGTGTCATCAATTCCTCCCGCTGTT 370
QY 81 TrpArgAspTyrTyrIleValIleValIleValTyrLeuValAspAlaValAspArg 100
D 371 TGGAAAGATTATATATCTAAGGTCGATGCTGTGTAATCTGATGATTCCTTGACAA 430
QY 101 GluArgPheAlaGluSerLysGluLeuAspSerLeuLeuSerLeuSerLeuSer 120
D 431 GAAAGGTTTGCAGAGGCCAAGAAAGAGCTGAGCTCTCTCTACGAGCTCTTGCA 490
QY 121 GlnValProValIleValIleGlyAsnLysIleAspIleProTyrAlaSerSerGluAsp 140
D 491 ACTGTTCTTCTTCTGATACCTGGTAAAGATTAAGACATCCCATATGCTGCTCAGAAAT 550
QY 141 GluLeuArgPheThrLeuGlyLeuThr--MetThrThrGlyLysGlyThrValAsnLeu 159
D 551 GAACCTCGTTACCATATGAGGCTTAACGAGGCTGACCACTGCGAAAGGAAAGTAACTCG 610
QY 160 GlyAspSerAsnIleArgProIleGluValPheMetCysSerIleValArgLysMetGly 179
D 611 GCAGATTCCAAATGTCGCTCCAGTTGAGGATTCATCTGACGATAGTCCGCAAAATGCGA 670
QY 180 TyrGlyGluGlyPheLeuTyrMetThrGlnTyrIleLys 192
D 671 TATGGAGAAAGGCTTCAATGATGATCTCAGTATATCAAG 709
Db
RESULT 9
ADM45760
ID ADM45760 standard; DNA; 830 BP.
AC ADM45760;
XX
DT 03-JUN-2004 (first entry)
DE Insect resistance associated DNA sequence SegID1167.
XX
KM Insect resistant phenotype; plant protectant; gene therapy;
KM Arabidopsis thaliana; Nicotiana benthamiana; Oryza sativa;
KM Papaver rhoeas; rice; insect resistance; insect-resistant plant; ds.
XX
```


OS Unidentified.
XX W02003020025-A2.
XX
PD 13-MAR-2003.
XX
XX 30-AUG-2002; 2002W0-US027882.
XX
XX 31-AUG-2001; 2001US-0316319P.
XX
XX (DOMC) DOM CHEM CO.
XX
XX Shukla V, Meade T, Larrinua I;
XX
XX WPI; 2003-290133/28.
XX
XX New isolated nucleic acid having expression that results in an insect
PT resistant phenotype, useful for conferring insect resistance and for
PT producing insect-resistant plants.
XX
XX Claim 1; SEQ ID NO 1167; 396pp; English.
XX
XX This invention relates to a novel isolated nucleic acid comprising, or
CC hybridising under low stringent conditions to, any of the 1214 nucleic
CC acid sequences given in the specification, where the expression of the
CC nucleic acid in a plant results in an insect resistant phenotype. The
CC invention may be useful as a plant protectant or for gene therapy. The
CC genes are derived from Arabidopsis thaliana, Nicotiana benthamiana, Oryza
CC sativa and pepper thasas. The isolated nucleic acid and vector are
CC useful for conferring insect resistance and for producing insect-
CC resistant plants. The present sequence is that of a DNA sequence of the
CC invention which may confer insect resistance to plants.
XX
XX Sequence 830 BP; 221 A; 165 C; 204 G; 240 T; 0 U; 0 Other;
SO
Alignment Scores:
Pred. No.: 2.69e-101 Length: 830
Score: 871.50 Matches: 161
Percent Similarity: 94.30% Conservative: 21
Best Local Similarity: 83.42% Mismatches: 10
Query Match: 87.32% Indels: 1
DB: 11 Gaps: 1
US-10-688-481-11 (1-192) x ADM45760 (1-830)
QY 1 MetPheLeuValAspTrpPheTyrGlyPheLeuAlaSerIleGlyLeuTrpGlnLysGlu 20
DB 150 ATGTTCTTGATGATGTTGTTCTATGGAATCTTACGCAACGCTCGGATTATGCGAGAGAG 209
QY 21 AlaIysIleLeuPheLeuGlyLeuAspAsnAlaGlyIleThrThrLeuLysIleMetLeu 40
DB 210 GCTAAGATCTTGTGTTTGGGCTCGATATATGCCGCCAABAACACCTTACTCATATGTTG 269
QY 41 LysAspGluLysLeuGlyGlnHisGlnProThrglnTyrProThrSerGlnLysSer 60
DB 270 AAAAGATGAGAGATTGTTCAACATCAGCCAAACACATATCCGACGTGAGAGAGCTTGT 329
QY 61 IleAsnAlaValLysPheLeuAlaPheAspLeuGlyGlyHisThrIleAlaArgArgVal 80
DB 330 ATCGCAAGATCAAGATTCAAGACATTGACTGGTGTGCATCAAAATGCTCGCCGTGTT 389
QY 81 TrpArgAspTyrTyrAlaIleValAspAlaIleValTyrLeuValAspAlaValAspArg 100
DB 390 TGGAAAGATTATTATGCTAAGGTCATGCTGTGTATCTTGTCGATTCCTTTGACAAA 449
QY 101 GluArgPheAlaGluSerIleLysGlnLeuAspSerIleLeuSerAspAspSerLeuSer 120
DB 450 GAAAGATTGCGAGATCCCAAGAAAGCTGATGCTGTCTCTGACGAGAGCTTGGCA 509
QY 121 GlnValProValLeuValLeuGlyLysnIleAspIleProTyrAlaSerSerGlnAsp 140
DB 510 ACTGTTCTTCTTCTGATACTGGGTAAACAAGATGACATCCCATATGCTGCTCAGAAAGAT 569

QY 141 GluLeuArgPheThrLeuGlyLeuThr---MetThrThGlyLysGlyThrValaenLeu 159
DB 570 GAACCTGCTTACCATATGCGGCTTACGAGCGCTACACCTGCAAGAGTAAACCTG 629
QY 160 GlyAspSerAsnIleArgProIleGluValAlaPheMetCysSerIleValArgLysMetGly 179
DB 630 GCAGATTCCAAATGTCGTCACGTTGAGGTTATTCATGTGACGCAATATCCGCAAAATGGCA 689
QY 180 TyrGlyGluGlyPheLysTrpMetThrGlnTyrIleLys 192
DB 690 TATGAGAAAGGCTTCAGATGATGATGCTCAGTATATCAAG 728
RESULT 10
ADK52065
ID ADK52065 standard; cDNA; 1164 BP.
XX
AC ADK52065;
XX
DT 21-APR-2005 (first entry)
XX
XX Plant full length insert polynucleotide seqid 26805.
DE
XX plant protectant; plant growth regulator; gene therapy; plant;
KM recombinant DNA construct; physical array; plant breeding marker;
KM cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KM extreme osmotic condition; pathogen tolerance; pest tolerance;
KM growth rate; cell cycle pathway; disease resistance;
KM galactomannan production; lignin production; plant growth regulator;
KM yield; plant growth; plant development; seed oil; protein yield;
KM protein content; gene; ss.
XX
XX Unidentified.
OS
XX US2004034888-A1.
XX
XX 19-FEB-2004.
XX
XX 28-APR-2003; 2003US-00425114.
XX
XX 06-MAY-1999; 99US-00304517.
XX
XX 05-NOV-2001; 2001US-00985678.
XX
XX (LIU/) LIU J.
XX (ZHOU/) ZHOU Y.
XX (KOVA/) KOVALIC D K.
XX (SCRE/) SCREEN S E.
XX (TABA/) TABASKA J E.
XX (CAO/) CAO Y.
XX
XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX
XX WPI; 2004-180133/17.
XX
XX New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
XX Claim 1; SEQ ID NO 26805; 15pp; English.
XX
XX The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.segdata.uspo.gov/sequence.html?DocID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake

CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This sequence represents a plant full length insect
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.

XX Sequence 1164 BP; 271 A; 262 C; 361 G; 270 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1,41e-100	Length:	1164
Score:	867.50	Matches:	161
Percent Similarity:	93.26%	Conservative:	19
Best Local Similarity:	83.42%	Mismatches:	12
Query Match:	86.92%	Indels:	1
DB:	13	Gaps:	1

US-10-688-481-11 (1-192) x ADM52065 (1-1164)

```
Qy 1 MetPheLeuValAspTrpPheTyrGlyPheLeuAlaSerIleGlyLeuTyrGlnIlyeGlu 20
Db 259 ATGTTCTGCTGACGACGCTTCTATGGGCTGCTGACCTGCTGAGCTTGGCAGAGAG 318
Qy 21 AlaIysIleLeuPheLeuGlyLeuAspAsnAlaGlyIlyeThrThrLeuLeuHismetLeu 40
Db 319 GCTAAGATCCTCTTCTTGGCTCTGACCAAGCCGGCAAGACCACTCTCCACATGCTG 378
Qy 41 LysAspGluIlyeLeuGlyGlnHismetProThrGlnTyrProThrSerGluIleuSer 60
Db 379 AAGACACAGCGGCTCGTACGACACACCCGACGACGACCCAGTACAGAGAGTTAGC 438
Qy 61 ILeAsnArgValIlyePheIlyeAlaPheAspLeuGlyIlyeThrIleAlaArgVal 80
Db 439 ATGCGCAGATCAAGCTTCAAGGCTTCACTTGGGGCCGCCAGACCCGCCGCCGCTC 498
Qy 81 TrpArgAspTyrTyrAlaIlyeValAspAlaIleValTyrLeuValAspAlaValAspArg 100
Db 499 TGGAGAGACTACTACGCAAGGTTGATGCTGTGTGATCTTGGTGTGATGCTTGAACAG 558
Qy 101 GluArgPheAlaGlySerIlyeGlyGluLeuAspSerIleuSerIleuSer 120
Db 559 GAACGTTTCCCGATCGAAGAGAGACCTTGATCCCTCTTGCAGATGACTCCCTTGCA 618
Qy 121 GluValProValLeuValLeuGlyAsnIlyeIleAspIleProTyrAlaSerSerGluAsp 140
Db 619 AACGTTCTTCTTCTTCACTGCGCACAAGATGACATCCCAACGCGGCTTCAAGAGAG 678
Qy 141 GluLeuArgPheThrLeuGlyLeuThr--MetThrThrGlyIlyeGlyThrValAsnLeu 159
Db 679 GAGCTGAGTACTACTCGGCTGAGCAACTTCAACACCGGAGAGGCAACGTGAATTCG 738
Qy 160 GlyAspSerAsnIleArgProIleGluValPheMetCysSerIleValArgIlyeMetGly 179
Db 739 GCGGACCTCCACAGCTCCGCCCTGAGATCTTCATGTCAGTGTGTGCGCAAGATGGGC 798
Qy 180 TyrGlyGlyGlyPheIlyeTyrMetThrGlnTyrIleIlys 192
Db 799 TATGGCGAAGGCTTCAATGATGTCTCAGTACATCAAG 837
RESULT 11
ADM45777 standard; DNA; 615 BP.
XX ADM45777;
XX AC
XX 03-JUN-2004 (first entry)
XX Insect resistance associated DNA sequence SegID1184.
XX Insect resistant phenotype; plant protectant; gene therapy;
XX Arabidopsis thaliana; Nicotiana benthamiana; Oryza sativa;
XX Papaver rhoeas; rice; insect resistance; insect-resistant plant; ds.
XX Unidentified.
```

XX
PN WO2003020025-A2.
XX
PD 13-MAR-2003.
XX
PF 30-AUG-2002; 2002WO-US027882.
XX
PR 31-AUG-2001; 2001US-016319P.
XX
PA (DOWC) DOW CHEM CO.
XX
PI Shukla V, Meade T, Larrinua I;
XX
DR WPI; 2003-290133/28.
XX
PT New isolated nucleic acid having expression that results in an insect
PT resistant phenotype, useful for conferring insect resistance and for
PT producing insect-resistant plants.
PS
PS Claim 1; SEQ ID NO 1184; 396bp; English.
XX
XX This invention relates to a novel isolated nucleic acid comprising, or
XX hybridizing under low stringent conditions to, any of the 1214 nucleic
XX acid sequences given in the specification, where the expression of the
XX nucleic acid in a plant results in an insect resistant phenotype. The
XX invention may be useful as a plant protectant or for gene therapy. The
XX genes are derived from Arabidopsis thaliana, Nicotiana benthamiana, Oryza
XX sativa and Papaver rhoeas. The isolated nucleic acid and vector are
XX useful for conferring insect resistance and for producing insect-
XX resistant plants. The present sequence is that of a DNA sequence of the
XX invention which may confer insect resistance to plants.

SQ Sequence 615 BP; 173 A; 105 C; 167 G; 170 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.03e-100	Length:	615
Score:	865.50	Matches:	162
Percent Similarity:	92.75%	Conservative:	17
Best Local Similarity:	83.94%	Mismatches:	13
Query Match:	86.72%	Indels:	1
DB:	11	Gaps:	1

US-10-688-481-11 (1-192) x ADM45777 (1-615)

```
Qy 1 MetPheLeuValAspTrpPheTyrGlyPheLeuAlaSerIleGlyLeuTyrGlnIlyeGlu 20
Db 29 ATGTTCTGCTGACGACGCTTCTATGGGCTGCTGACCTGCTGAGCTTGGCAGAGAG 88
Qy 21 AlaIysIleLeuPheLeuGlyLeuAspAsnAlaGlyIlyeThrThrLeuLeuHismetLeu 40
Db 89 GCGAAGATATGTTTCTTGAAGCTTGAATGCTGCGCAACCACTTGTCTTCAATGTTG 148
Qy 41 LysAspGluIlyeLeuGlyGlnHismetProThrGlnTyrProThrSerGluIleuSer 60
Db 149 AAGAGACAGAGATTTGGTGGACGATCAACCTACCAATACCAACATCAGAGAGTGTAGT 208
Qy 61 ILeAsnArgValIlyePheIlyeAlaPheAspLeuGlyIlyeThrIleAlaArgVal 80
Db 209 ATAGGTAAATTAAGTTCAGAGCTTTGATTTGAGAGACCAAAATGCTTAGAAGATC 268
Qy 81 TrpArgAspTyrTyrAlaIlyeValAspAlaIleValTyrLeuValAspAlaValAspArg 100
Db 269 TGGAGAGACTACTACTCGGCTGAGCAAGTGTGCTTCACTTGTATGCTTACAGACCA 328
Qy 101 GluArgPheAlaGlySerIlyeGlyGluLeuAspSerIleuSerIleuSer 120
Db 329 GAGAGGTTTCCCGAGTCAAGAGAGATGATGAGGCTTCTTCAGATGATCATTTGCA 388
Qy 121 GluValProValLeuValLeuGlyAsnIlyeIleAspIleProTyrAlaSerSerGluAsp 140
Db 389 AATGTCATCTTCTTCTTGGGAAACCAAGATGATATACATATGCTGCTTCAAGAGAC 448
Qy 141 GluLeuArgPheThrLeuGlyLeuThr--MetThrThrGlyIlyeGlyThrValAsnLeu 159
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|||||:::|||||:::|||||
Db 449 GAGTCGTTATCACTTGGCGCTTAAGTGTGTGACCACTGGCAAGGCTAAAGTCAACCTC 508
Qy 160 G[AspSer]anileArgProIleGluValPheMetCysSerIleValArgIleMetGly 179
Db 509 GCTGGTCAAAATGTCCTTCATTCAGATGTTATGTGCAAGCATTTGTGCGCAAGATGGGA 568
Qy 180 TyrGlyGluGlyPheIleTyrPheMetThrGlnTyrIleIys 192
Db 569 TATGTGAGGCGCTTCAAGTGTGATGTCCGAATACATCAAG 607
RESULT 12
ADR60523
ID ADR60523 standard; cDNA; 1047 BP.
XX
AC ADR60523;
XX
DT 02-DEC-2004 (first entry)
XX
DE Cotton cDNA sequence, SEQ ID 1304.
XX
KM Cotton; ss; plant; cold tolerance; growth rate; cell cycle pathway;
KM drought tolerance; plant disease resistance; galactomannan; lignin;
KM plant growth regulator; heat tolerance; herbicide tolerance;
KM homologous recombination; extreme osmotic condition tolerance;
KM pathogen resistance; pest resistance; yield; photosynthesis; seed oil;
KM stress resistance.
XX
OS Gossypium hirsutum.
XX
PN US2004181830-A1.
XX
PD 16-SEP-2004.
XX
PE 29-JAN-2004; 2004US-00767795.
PR 07-MAY-2001; 2001US-00849529.
PR 12-DEC-2001; 2001US-00021323.
XX
PA (KOVA/) KOVALIC D K.
PA (ZHOU/) ZHOU Y.
PA (CAO/) CAO Y.
PI Kovalic DK, Zhou Y, Cao Y;
PI
XX KPI; 2004-667716/65.
DR
XX
XX New recombinant nucleic acid molecules and polypeptides from Gossypium
PT hirsutum, useful for producing plants with improved biological
PT characteristics (e.g. improved plant cold or drought tolerance).
XX
PS Claim 1; SEQ ID NO 1304; 14pp; English.
XX
XX The invention relates to a recombinant polynucleotide comprising any of
CC the 58798 Cotton plant cDNA sequences mentioned in the specification.
CC Also a recombinant polypeptide comprising any of the 58798 amino acid
CC sequences mentioned in the specification and producing a plant having an
CC improved property. Producing a plant having an improved property
CC comprises transforming a plant with a recombinant construct comprising a
CC promoter region functional in a plant cell operably joined to a
CC polynucleotide comprising a coding sequence for a polypeptide associated
CC with the property, and growing the transformed plant. The polypeptide is
CC useful for improving plant cold tolerance, manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, improving plant
CC drought tolerance, providing increased resistance to plant disease,
CC producing galactomannan (or lignin or plant growth regulators), improving
CC plant heat tolerance, improving plant tolerance to herbicides, increasing
CC the rate of homologous recombination in plants, improving plant tolerance
CC to extreme osmotic conditions or to pathogens or pests, improving yield
CC by modification of photosynthesis, modifying seed oil or protein yield
CC and/or content, improving yield by modification of carbohydrate, nitrogen
CC or phosphorus use and/or uptake, or improving yield by providing improved
CC plant growth and development under at least one stress condition. The

CC polynucleotide and polypeptide may also be used in recombinant DNA
CC constructs, in physical arrays of molecules, as plant breeding markers,
CC or in computer-based storage and analysis systems. The present sequence
CC is a Cotton plant cDNA of the invention. NOTE: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?docid=20040181830. However only 6585
CC polynucleotide sequences were available, the remaining 52213
CC polynucleotides and all 58798 protein sequences were not present.
XX
SO Sequence 1047 BP; 272 A; 217 C; 236 G; 322 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 2,94e-100 Length: 1047
Score: 864.50 Matches: 160
Percent Similarity: 93.78% Conservative: 21
Best Local Similarity: 82.90% Mismatches: 11
Query Match: 86.62% Indels: 1
DB: 13 Gaps: 1
US-10-688-481-11 (1-192) x ADR60523 (1-1047)
Qy 1 MetPheIleuValAspTyrPheTyrGlyPheIleuValSerIleGlyLeuTyrGlnIysGlu 20
Db 221 ATGTTCTTTGGATTGGTTCTATAGTGTTCTTGTCTTCCCTGTGCTATGGCAGAAAGAG 280
Qy 21 A[Ala]ysIleLeuPheLeuGlyIleuAspAsn[Ala]GlyThrThrLeuLeuH[Met]Leu 40
Db 281 GCTTAAGATCTTGTTCCTCGGCTTCGATACGCCGCGAAACCACTTGCTTCATATGTTA 340
Qy 41 LysAspGluLysLeuGlyGlnH[Ser]GlnProThrGlnTyrProThrSerGluGluLeuSer 60
Db 341 AAAGACGAGAGATTGGTTCAACATCACGCCAACTCAGATCCCATGCGAAGACCTTAAT 400
Qy 61 IleAsnArgValIysPheIysAlaPheAspLeuGlyValIleThrIleAlaArgArgVal 80
Db 401 ATTGGAAATCAAGTTCAAAGCTTTGATTGGGTGCTCATGATTGCTGTCAGATC 460
Qy 81 TyrArgAspTyrTyrAlaIysValAspAlaIleValTyrLeuValAspAlaValAspArg 100
Db 461 TGGAAAGATTACATTCATGCTAAGTGGATGCTGTGTGATCCGTGATGATGCTCATGATGATA 520
Qy 101 GluArgPheAlaGluSerIysLysGluLeuAspSerLeuLeuSerAspAspSerLeuSer 120
Db 521 GAGAGTTTGCAAGATCGAAGAAAGAAAGAACTCGATCCCTGCTTCAGACGAGCCCTTGCC 580
Qy 121 GlnValProValIleuValIleuGlyAsnIleIleAspIleProTyrAlaSerSerGluAsp 140
Db 581 AATGTCCGTTCTTATCTTATCGAAGAAAGATCGATATACATACGCTGCTCGAGAGAT 640
Qy 141 GluLeuArgPheThrLeuGlyLeuThr---MetThrThrGlyLysGlyThrValAsnLeu 159
Db 641 GAATTACGTTACCACTCCGCGCTCACAACTTTCACAGGCGGAGGGAAGGTBAACCTA 700
Qy 160 G[AspSer]anileArgProIleGluValPheMetCysSerIleValArgIleMetGly 179
Db 701 GCAACATCGAATGCGCGCTCCGCTAGAGATATTATGTGCGACATATGCCGCAAAATGGGA 760
Qy 180 TyrGlyGluGlyPheIleTyrPheMetThrGlnTyrIleIys 192
Db 761 TATGGGAGCGGCTTAAAGTGTGATGTCCAGATATCAAG 799
RESULT 13
ACU34445
ID ACU34445 standard; cDNA; 876 BP.
XX
XX ACU34445;
XX
DT 02-JUN-2005 (first entry)
XX
DE Rice abiotic stress response related polynucleotide SEQ ID NO:13008.
XX
KM ss; abiotic stress tolerance; transgenic plant; plant; cereal;

KW agriculture.
XX
OS Oryza sativa.
XX
PN WO2003008540-A2.
XX
PD 30-JAN-2003.
XX
PF 21-JUN-2002; 2002WO-US019668.
XX
PR 22-JUN-2001; 2001US-0300112P.
PR 24-AUG-2001; 2001US-0314662P.
PR 26-SEP-2001; 2001US-0325272P.
PR 21-NOV-2001; 2001US-0332132P.
XX
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
PI Krepe J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F;
PI Moughamer T, Provart N, Riecke D, Zhu T;
XX WPI; 2003-248011/24.
XX
XX New stress-responsive nucleic acid, useful for altering the
PT responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold
PT stress, salt stress or osmotic stress.
XX
XX Claim 48; SEQ ID NO 13008; 89pp; English.
XX
XX The invention relates to novel abiotic stress responsive polynucleotides
CC and polypeptides. Also disclosed are vectors, expression cassettes, host
CC cells, and plants containing such polynucleotides. Also disclosed are
CC methods for using the polynucleotides and polypeptides to alter the
CC responsiveness of a plant to abiotic stress. The invention is useful in
CC agriculture. The nucleic acid is useful for determining whether a test
CC plant has been exposed to an abiotic stress condition. It is also useful
CC for selecting an agent that alters abiotic stress regulated
CC polynucleotide expression in a plant cell, and to identify a homolog or
CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid
CC molecule and the polypeptide encoded by it are useful in altering the
CC responsiveness of a plant to an abiotic stress, such as cold stress, salt
CC stress, osmotic stress or any of their combinations. The present sequence
CC is used in the exemplification of the invention
XX
SQ Sequence 876 BP; 196 A; 269 C; 240 G; 171 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 4.11e-100 Length: 876
Score: 862.50 Matches: 160
Percent Similarity: 93.78% Conservative: 21
Best Local Similarity: 82.90% Mismatches: 11
Query Match: 86.42% Indels: 1
DB: 11 Gaps: 1
US-10-688-481-11 (1-192) x ALCJ4445 (1-876)
QY 1 MetPheLeuValAspTrpPheTyrGlyPheLeuAlaSerIleGlyLeuTrpGlnLeuSerGln 20
Db 298 ATGTTCTCTGGAGACTGCTCTTACGCGGCTCTGCTCCCTCGCTCGCAAGAGAG 357
QY 21 AlaValIleLeuPheLeuGlyLeuAspAsnAlaGlyIleValThrIleLeuLeuHISmetLeu 40
Db 358 GCGAAGATCTCTTCTCGGCTCTGACACGCGGCAAGACACGCTGCTCCACATGCTC 417
QY 41 LysAspGluValLeuGlyGlnHisGlnProThrGlnTyrProThrSerGluGluLeuSer 60
Db 418 AAGGACGAGGGTGGTGGTGGACGACCAAGCCGACGACCGAGCTCGAGGAGCTAGC 477
QY 61 IleAsnArgValIleValPheLeuValAlaPheAspLeuGlyIleValIleValIleValIleVal 80
Db 478 ATCGCAAGATCAAGTCAAGGCTTGCAGCTCGGCGGCAACGATCGGCGCGCTC 537
QY 81 TrpArgAspTyrTyrAlaValValAspAlaIleValTyrLeuValAspAlaValAspArg 100

Db 538 TGGAAGATTACTACGCAAAAGTTGATGCTGTAGTATACCTGGTAGATGCTATGATAG 597
QY 101 GluArgPheAlaGluSerIleValSerIleLeuAspSerLeuLeuSerAspAspSerLeuSer 120
Db 598 GAGCGATTTGCTGAATCAAAAAAGAGCTGACGCTCTCTGTCATATATTCCTTGCCA 657
QY 121 GlnValProValLeuValLeuGlyAenValIleAspIleProTyrAlaSerSerGluAsp 140
Db 658 AATGTTCCATTTCTCATCTCTGCGCAACGATGATATCCGATATCTGCTGGAAG 717
QY 141 GluLeuArgPheThrLeuGlyLeuThr---MetThrThrGlyLeuGlyThrValAsnLeu 159
Db 718 GAGCTCGGATATCACCTTAGAGCTTACCACTTCAACCGGGAAGGCAAGTCAACCTT 777
QY 160 GlyAspSerAsnIleArgProIleGluValPheMetCysSerIleValArgIleMetGly 179
Db 778 GCGACTCCAAATGTCGCGCCTTAGAGTTTTCATGTGAGTGTGTGCAAGATGGC 837
QY 180 TyrGlyGluGlyPheLeuTrpMetThrGlnTyrIleLeu 192
Db 838 TACGCGATGCTTCAAGTGGTCTCCCAATCATCATAG 876
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ID AAC42538 strand; DNA; 885 BP.
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XX AAC42538;
XX
XX 17-OCT-2000 (first entry)
XX
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 35935.
XX
XX Hybridization assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
XX promoter; termination sequence; ss.
XX
XX Arabidopsis thaliana.
XX
XX EPI033405-A2.
XX
XX 06-SEP-2000.
XX
XX
XX 25-FEB-2000; 2000EP-00301439.
XX
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XX 25-FEB-1999; 99US-0121825P.
XX 05-MAR-1999; 99US-0123180P.
XX 09-MAR-1999; 99US-0123548P.
XX 23-MAR-1999; 99US-0125788P.
XX 25-MAR-1999; 99US-0126264P.
XX 29-MAR-1999; 99US-0126785P.
XX 01-APR-1999; 99US-0127462P.
XX 06-APR-1999; 99US-0128234P.
XX 08-APR-1999; 99US-0128714P.
XX 16-APR-1999; 99US-0129845P.
XX 19-APR-1999; 99US-0130077P.
XX 21-APR-1999; 99US-0130449P.
XX 23-APR-1999; 99US-0130510P.
XX 28-APR-1999; 99US-0130891P.
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XX 05-MAY-1999; 99US-0132485P.
XX 06-MAY-1999; 99US-0132486P.
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PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
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PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
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PR 18-JUN-1999; 99US-0139750P.
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PR 21-JUN-1999; 99US-0139817P.
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PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
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PR 21-JUL-1999; 99US-0145088P.
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PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 28-JUL-1999; 99US-0145951P.
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PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
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PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
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PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
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PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161040P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.

PR 26-OCT-1999; 99US-0161361P.
 PR 28-OCT-1999; 99US-0161920P.
 PR 28-OCT-1999; 99US-0161992P.
 PR 28-OCT-1999; 99US-0161993P.
 PR 29-OCT-1999; 99US-0162142P.

Alignment Scores:

Pred. No.:	4,17e-100	Length:	885
Score:	862.50	Matches:	160
Percent Similarity:	93.78%	Conservative:	21
Best Local Similarity:	82.90%	Mismatches:	11
Query Match:	86.42%	Indels:	1
DB:	3	Gaps:	1

US-10-688-481-11 (1-192) x AAC42538 (1-885)

QY 1 MetPheLeuValAspTyrPheTyrGlyPheLeuAlaSerIleGlyLeuTyrGlyVal 20
 Db 94 ATGTTATCATGATCGATTGTTCTATGGCGTTCTCGCTTCGTATAGGTTATCGAGAAAGAG 153
 QY 21 AlAluylleuPheLeuGlyLeuAspAsnAlaGlylysthrThrleuLeuHlmetleu 40
 Db 154 GCTAAGATCTTGTTCGGACCTCGATTAATGCTGTAACCACTCTGCTTCACTGTTG 213
 QY 41 LysAspGluIuylsleuGlyGlnHlsglnProThrGlnTyrProThrSerGlyGluLeuSer 60
 Db 214 AAGAGACAGAGATTTGTTACGATCAGCATCAGCATCAGCATCAGCATCAGCATCAGCATCAGC 273
 QY 61 LLeAsnArgValIlyspPheLyAlaPheAspLeuGlyGlyHlsthrlleAlaArgArgVal 80
 Db 274 ATGGGAAATCAAGATTAAAGGCTTTGATTGGGTGTCACAGATTGCTCGAGGCTC 333
 QY 81 TrpArgAspTyrTyrAlaIlyValAspAlaIleValTyrleuValAspAlaValAspArg 100
 Db 334 TGGAGAGATTACTATGCTTAAGTGGACGCTGCTGCTTACCTAGTGTGCTTACGACAA 393
 QY 101 GluArgPheAlaGlyserlysllyGluLeuAspSerleuSerAspAspSerleuSer 120
 Db 394 GAGAGATTTCAGATCAAAAGAAAGAACTGATGACATCTCTTCAGCGAATCCCTTACC 453
 QY 121 GlnValProValIleuValIleuGlyAsnIlyleAspIleProTyrAlaSerSerGlyuAsp 140
 Db 454 AGGTTCCATTTCCTCATTCATGAGAAACAGATGACATACGATGTCATGACAGAC 513
 QY 141 GluLeuArgPheThrleuGlyLeuThr--MetThrThrGlylyGlyThrValAsnLeu 159
 Db 514 GAGCTCGTTCACCATCTCGGCTCTCCACTTCACTACAGAAAGGCTAAAGTCAATCTA 573
 QY 160 GlysAspSerAsnIleArgProIleGluValPheMetCysSerIleValArgIysMetGly 179
 Db 574 ACGGATTCGAACGTTAGCCATTCGAGGTTTCAATGTCAGCATTCGACGAAATGGGT 633
 QY 180 TyrGlyGluGlyPheLystrMetThrGlnTyrIleIys 192
 Db 634 TACGAGAAAGTTTCAATGCGTTCTCAATACATCAAG 672
 RESULT 15
 ABK71577 standard; cDNA; 928 BP.
 AC ABK71577;
 XX 30-JUL-2002 (first entry)
 XX Human dlchp polynucleotide #43.
 XX Human; dlchp; diagnostic and therapeutic polynucleotide; gene; ss; bone;
 KM cell proliferative disorder; cancer; tumour; autoimmune disorder; brain;
 KM inflammatory disorder; viral infection; bacterial infection; seizure;
 KM fungal infection; parasitic infections; developmental disorder; breast;
 KM endocrine disorder; metabolic disorders; neurological disorder; cervix;
 KM gastrointestinal disorder; transport disorder; gene therapy; kidney;
 KM adrenal gland; bone marrow; lung; ovary; pancreas; prostate; spleen;

KM skin; testis; thymus.
 XX
 OS Homo sapiens.
 XX
 PN WO200220754-A2.
 XX
 PD 14-MAR-2002.
 XX
 PF 29-AUG-2001; 2001MO-US027127.
 XX
 PR 05-SEP-2000; 2000US-0229747P.
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 PR 05-SEP-2000; 2000US-0229748P.
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 PR 05-SEP-2000; 2000US-0229749P.
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 PR 05-SEP-2000; 2000US-0229750P.
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 PR 05-SEP-2000; 2000US-0229751P.
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 PR 05-SEP-2000; 2000US-0230583P.
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 PR 06-SEP-2000; 2000US-0230585P.
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 PR 06-SEP-2000; 2000US-0230514P.
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 PR 06-SEP-2000; 2000US-0230515P.
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 PR 06-SEP-2000; 2000US-0230518P.
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 PR 06-SEP-2000; 2000US-0230519P.
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 PR 06-SEP-2000; 2000US-0230597P.
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 PR 06-SEP-2000; 2000US-0230598P.
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 PR 06-SEP-2000; 2000US-0230599P.
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 PR 06-SEP-2000; 2000US-0230610P.
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 PR 06-SEP-2000; 2000US-0230656P.
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 PR 07-SEP-2000; 2000US-0230951P.
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 PR 07-SEP-2000; 2000US-0231163P.
 XX
 PR 07-SEP-2000; 2000US-0231167P.
 XX
 PA (INCYTE) INCYTE GENOMICS INC.
 XX
 PI Stuart J, Lincoln SE, Altus CM, Dufour GE, Chalup MS, Hillman JR;
 PI Jones AU, Yu JY, Wright RJ, Gietzen D, Liu TF, Yap PB, Dahl CR;
 PI Montyama MG, Bradley DL, Rohatgi SD, Harris B, Roseberry AM;
 PI Gerstein EH, Peralta CH, David MH, Panzer SR, Flores V, Dafio A;
 PI Marwaha R, Chen AJ, Chang SC, Au AP, Imman RR;
 XX
 DR WPI; 2002-383054/41.
 DR P-PDB; ABG59985.
 XX
 PT An isolated polynucleotide useful in diagnostics and therapeutics.
 XX
 PS Claim 1; Page 427; 686pp; English.
 XX
 CC The invention relates to human diagnostic and therapeutic (dlchp)
 CC polynucleotides and their associated polypeptides (DTRP polypeptides) of
 CC the sequences of the invention are used in the treatment and diagnosis of
 CC cell proliferative disorders (e.g. atherosclerosis, cirrhosis), cancers
 CC (e.g. tumours of the adrenal gland, bone, bone marrow, brain, breast,
 CC cervix, kidney, lung, ovary, pancreas, prostate, skin, spleen, testis or
 CC thymus), autoimmune/inflammatory disorders (e.g. asthma, bronchitis,
 CC psoriasis, osteoporosis), viral infections, bacterial infections, fungal
 CC infections, parasitic infections, developmental disorders (e.g. anaemia,
 CC epilepsy), seizure disorders (e.g. cerebral palsy, spina bifida),
 CC endocrine disorders (e.g. thrombosis, aneurysm), metabolic disorders
 CC (e.g. obesity, diabetes), neurological disorders (e.g. stroke,
 CC amyotrophic lateral sclerosis, multiple sclerosis), gastrointestinal
 CC disorders (e.g. ulcerative colitis, lymphoma) and transport disorders
 CC (e.g. myotonic dystrophy, catatonis, peripheral neuropathy). Sequences
 CC ABK71535-ABK71809 represent human dlchp polynucleotides of the invention
 XX
 SQ Sequence 928 BP; 206 A; 251 C; 262 G; 209 T; 0 U; 0 Other;
 XX
 Alignment Scores:
 Pred. No.: 4.46e-100 Length: 928
 Score: 862.50 Matches: 160
 Percent Similarity: 93.78% Conservative: 21
 Best Local Similarity: 82.90% Mismatches: 11
 Query Match: 86.42% Indels: 1

DB:	6	Gaps:	1
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US-10-688-481-11 (1-192) x ABK71577 (1-928)

QY 1 MetPheLeuValAspTrpPheTyrGlyPheLeuAlaSerIleGlyLeuTProGlnLysGlu 20
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QY 21 AlaValIleLeuPheLeuGlyLeuAspAsnAlaGlyLysThrThrLeuLeuHisMetLeu 40
Db 223 GCCAAGATCTCTTCTGTCGGCTCGACCAAGCGGGCAAGCCAGCGTGTCCACATGTCTC 282
QY 41 LysAspGlyLysLeuGlyGlnHisGlnProThrGlnTyrProThrSerGlyGluLeuSer 60
Db 283 AAGGACGAGCGGTGGTGGCAGACCAGCGGACCCAGACCCGACGTGGAGGAGCTCAGC 342
QY 61 IleAsnArgValLysPheLysAlaPheAspLeuGlyGlyHisThrIleAlaArgVal 80
Db 343 ATCGGCACATACAGTTCACAGGGGTTCGACTTGGGGCCACCAAGATGGCGCCGGGTG 402
QY 81 TrpArgAspTyrTyrAlaLysValAspAlaIleValTyrLeuValAspAlaValAspArg 100
Db 403 TCGAAGGATTACTACCCAAAGGTGATGCTGTAGTATACCTGGTAAATGATGATTAAG 462
QY 101 GluArgPheAlaGluSerLysLysGluLeuAspSerLeuLeuSerAspAspSerLeuSer 120
Db 463 GAGCAGATTGTGGAATCAAGAAGAGAGCTCGAGTGCCTCTGTCGTATGATTTCTTTGGCC 522
QY 121 GlnValProValLeuValLeuGlyAsnLysIleAspIleProTyrAlaSerSerGluAsp 140
Db 523 AATGTTCATTTCTCTACTCTGGCAACAGATTTAGATCCCATATGCTGTCTTGAAGAG 582
QY 141 GluLeuArgPheThrLeuGlyLeuThr---MetThrThrGlyLysGlyThrValAsnLeu 159
Db 583 GAGCTACGGTATCACCTTAGCGCTTACCACTTACCAACCGGAAAGGCCAAGTCAACCTT 642
QY 160 GlyAspSerAsnIleArgProIleGlyValPheMetCysSerIleValArgLysMetGly 179
Db 643 GCGCACTCCAAATGTCCGTCCACTTGAGGTCTTCATGTGCAGTGTGTGTTCCAGATGGGC 702
QY 180 TyrGlyGluGlyPheLysTrpMetThrGlnTyrIleLys 192
Db 703 TACGGTGATGTTCAAGTGGGTCTCCCAAGTATCATCAAG 741

Search completed: December 9, 2005, 01:50:23
Job time : 473 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 9, 2005, 01:39:43 ; Search time 3745 Seconds
(without alignments)
2398.697 Million cell updates/sec

Title: US-10-688-481-11
Perfect score: 998
Sequence: 1 MFLVDFWFGYGLASIGLWKE.....SIVRKKGYGEGFKMTQYIK 192

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 23393541228 residues
Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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4: gb_hic:*
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8: gb_esc7:*
9: gb_esc8:*
10: gb_esc9:*
11: gb_esc10:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	974	97.6	607	3	BJ952512 BJ952512
C 2	974	97.6	650	3	BJ599136 BJ599136
C 3	974	97.6	734	3	BJ598350 BJ598350
C 4	974	97.6	740	3	BJ609449 BJ609449
5	880.5	88.2	638	5	BJ0037417 946138F10
6	880.5	88.2	669	5	BJ0098049 946138F11
7	880.5	88.2	720	7	C0526683 3530_1_17

C 8	880.5	88.2	724	5	BQ779008	BQ779008 946116C06
9	880.5	88.2	749	3	BJ572166	BJ572166 BJ572166
10	880.5	88.2	830	3	DR829325	DR829325 2M_BPB007
11	880.5	88.2	877	8	DR824574	DR824574 2M_BPB006
12	880.5	88.2	903	7	CO443833	CO443833 M2CCL1006
13	880.5	88.2	1098	4	AY106333	AY106333 2aa may
14	880.5	88.2	861	7	CN206979	CN206979 TOR739 Ga
15	877.5	87.2	807	8	DN152566	DN152566 5207_C08
16	870.5	87.2	622	7	CV300967	CV300967 ESTH8831C
17	868.5	87.0	734	7	CV472407	CV472407 45743_1 C
18	868.5	87.0	793	5	BM688373	BM688373 BM688373
19	868.5	87.0	800	2	BG887826	BG887826 EST513077
20	868.5	87.0	882	2	BF460011	BF460011 071G06 Ma
21	868.5	87.0	885	8	DN168126	DN168126 LH_EA02M
22	867.5	86.9	755	8	CV724867	CV724867 EST5007_2
23	866.5	86.8	650	5	CA015435	CA015435 HT14E23r
24	866.5	86.8	673	3	BU226471	BU226471 BU226471
25	866.5	86.8	682	5	BQ839446	BQ839446 WHE416_B
26	866.5	86.8	692	5	BQ805647	BQ805647 WHE3569_D
27	866.5	86.8	700	1	AL505462	AL505462 AL505462
28	866.5	86.8	700	5	BQ471183	BQ471183 HVO1H06T
29	866.5	86.8	708	6	CD669290	CD669290 AZ02_111B
30	866.5	86.8	724	6	CA174544	CA174544 SC0FST101
31	866.5	86.8	783	7	CK123056	CK123056 BS8182410
32	866.5	86.8	1159	8	DR740572	DR740572 FGAS00051
33	865.5	86.7	629	2	BG350081	BG350081 083D01 Ma
34	865.5	86.7	646	2	BE494747	BE494747 WHE1272_G
35	865.5	86.7	675	5	BQ407022	BQ407022 GA_EA010
36	865.5	86.7	695	6	CD880780	CD880780 F1_075N23
37	865.5	86.7	702	3	BQ112215	BQ112215 EST597791
38	865.5	86.7	728	3	BI434155	BI434155 EST536916
39	865.5	86.7	735	2	DR035154	DR035154 18581_2 S
40	865.5	86.7	758	6	CD905083	CD905083 GA68_100H
41	865.5	86.7	834	7	CV302973	CV302973 75006_1 S
42	865.5	86.7	859	1	AJ822454	AJ822454 A822454
43	864.5	86.6	589	6	CA825610	CA825610 R62D03 tw
44	864.5	86.6	636	5	BU827781	BU827781 K008P84P
45	864.5	86.6	642	8	DN180683	DN180683 HO26G225

ALIGNMENTS

RESULT 1
BJ952512/c 607 bp mRNA linear EST 14-JUN-2005
LOCUS BJ952512 phnf full-length cDNA library Physcomitrella patens subsp.
DEFINITION BJ952512 patens cDNA clone phnf1p22 3', mRNA sequence.
ACCESSION BJ952512
VERSION BJ952512.1 GI:67692279
KEYWORDS EST.
SOURCE Physcomitrella patens subsp. patens
ORGANISM Physcomitrella patens subsp. patens
Bryophyta; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella;
1 (bases 1 to 607)
Fujita,T., Nishiyama,T., Shin-i,T., Kohara,Y. and Hasebe,M.
Physcomitrella patens subsp. patens
division of protoplasts
Unpublished (2005)
Contact: Tadao Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@gene.nig.ac.jp

Protoplasts were isolated from the protoplasts, further incubated at 25C under continuous light for 2-3 days. The regenerated cells, which were rich in cells at a stage during the first asymmetric cell division, were collected. Total RNA was extracted for constructing a full-length cDNA library. The database of the EST clones is available at the PhyscoBase (<http://moss.nibb.ac.jp>).

```

FEATURES
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        Location/Qualifiers
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                /organism="Physcomitrella patens subsp. patens"
                /mol_type="mRNA"
                /sub_species="patens"
                /db_xref="taxon:145481"
                /clone="pPh15p22"
                /tissue_type="regenerated protoplasts (chloronemata)"
                /dev_stage="at the first asymmetric cell division of
                protoplasts"
                /clone_libs="pPhf full-length cDNA library"
                /note="Protonemata were inoculated on BCD49G medium for
                every ca. 5 days. Protoplasts were isolated from the
                protonemata, further incubated at 25C under continuous
                light for 2-3 days. The regenerated cells, which were rich
                in cells at a stage during the first asymmetric cell
                division, were collected. Total RNA was extracted for
                constructing a full-length cDNA library."

ORIGIN
Alignment Scores:
Pred. No.: 3,286-115 Length: 607
Score: 974.00 Matches: 186
Percent Similarity: 98.96% Conservative: 4
Best Local Similarity: 96.88% Mismatches: 2
Query Match: 97.60% Indels: 0
Gaps: 3
DB: 3

US-10-688-481-11 (1-192) x BU592512 (1-607)

Qy 1 MetPheLeuValAapTTPheTYGlyPheLeuAAserIlegIleuTTPGlnLysGlu 20
Db 580 ATGTTTATCGTAGATTGCTTTATAGCTTCTTCGAGCAATAGCTTGTGCAAGAGAG 521
Qy 21 AlAlaValIleLeuPheLeuGlyLeuAspAsnAAGlyLeuThrThrLeuLeuHISMetLeu 40
Db 520 GCCAAATCTGTCTCGGTCTTGACATCCGGAAGAGACACTTCTGCACATGCTC 461
Qy 41 LysAspGluLysLeuGlyGlnHISGlnProThrgIntYrProThrSerGluGluLeuSer 60
Db 460 AAGCATGAGAACTCGGGCAACATCAACACGACAGTATCCAACTCGAAGATTGAGC 401
Qy 61 IleAsnArgValLysPheLysAlaPheAspLeuGlyGlyHISThrIleAlaArgVal 80
Db 400 ATCAATAGGTGAGATTCAAGACATTCGATCTAGGTGTCACAGATTGCTCGACGTGTG 341
Qy 81 ThrArgAspTYrTYrAlaLysValAspAlaIleValTYrLeuValAspAlaValAspArg 100
Db 340 TGGAGGAGACTACTATGCTTAAGGTGATGCTATCTTTACCTTTCGACGAGTTGACAG 281
Qy 101 GluArgPheAlaGluSerLysLysGluLeuAspSerLeuLeuSerAspAspSerLeuSer 120
Db 280 GAGAGGTTTCTCGAATCAAAAGAAAGAACTCCATCTTGTCTCGATGATCTCCCTCTCC 221
Qy 121 GlnValProValLeuValLeuGlyAsnLysIleAspIleProTYrAlaSerSerGluAsp 140
Db 220 CAAGTCTGCTGTGCTCTTGGCAACAAGATTGACATCCCTTACGCTGCCGAGAT 161
Qy 141 GluLeuArgPheThrLeuGlyLeuThrThrThrGlyLysGlyThValAsnLeuGly 160
Db 160 GAATTCGCGTACACCTCGGCTGACCATGACCAATGGCAAGAAAGCGTAACCTTAAG 101
Qy 161 AspSerAsnIleArgProIleGluValPheMetCysSerIleValArgLysMetGlyTYr 180
Db 100 GATAGCAACATCCGGCCCATTTGAGGTTTTCATGTGCATATAGTCCGTAATGGGTTAC 41
Qy 181 GlyGluGlyPheLysTYrMetThrGlnTYrIleLys 192
Db 40 GCGCAAGGCTCAAGTGTGATGACGCAATATTTAA 5

RESULT 2
BU59136/c BU599136 650 bp mRNA linear EST 22-OCT-2003
LOCUS

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DEFINITION
BU599136 normalized full length cDNA library, chloronemata,
caulonemata and rhizoid-like protonemata Physcomitrella patens
subsp. patens cDNA clone pPhn25113 3', mRNA sequence.

ACCESSION
BU599136
VERSION
BU599136.1 GI:37641128
KEYWORDS
EST.
SOURCE
Physcomitrella patens subsp. patens
ORGANISM
Physcomitrella patens subsp. patens
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
REFERENCE
1 (bases 1 to 650)
Nishiyama,T., Fujita,T., Shin-I,T., Seki,M., Nishide,H.,
Uchiyama,T., Kamiya,A., Carninci,P., Hayashizaki,Y., Shinozaki,K.,
Kohara,Y. and Hasebe,M.
Comparative genomics of Physcomitrella patens gametophytic
transcriptome and Arabidopsis thaliana: implication for land plant
evolution
Proc. Natl. Acad. Sci. U.S.A. 100 (13), 8007-8012 (2003)
JOURNAL
PUBMED
12808149
COMMENT
Contact: Tadaasu Shin-I
Center For Genetic Resource Information
National Institute of Genetics
111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp
A backbone of the vector is basically from pBluescript II (KS),
that was in vivo excised from a 1-F1C phage vector (Carninci et al.,
2001). 5' end of the cDNA that was digested with XhoI was ligated
to SalI site of the vector and the 3' end including polyA tail was
ligated to BamHI site of the
vector(5'- GAGAGAGAGAGATCCACCTG9AGAGTTTTTTTTTTTTTTVN-3' was
used as a 1st 3' primer, and
5'-GGTTCGAGTCATCGCTGTCCAGACGATGACTCGAAGACGNNNNN-3' as 2nd
5'-hairpin primer giving the following 5' boarder sequence,
AGGCCAATCGCCGACGATTCGATTCGAGAACCG). cDNA insert could be
amplified with conventional T7 and T3 primers. This full-length
cDNA library was generated according to the method described in
Nishiyama et al. (2003).
Protonemata were blended by the POLYTRON, and then cultivated on
the BCD49G medium for 13-14 days under the continuous light.
These clones are available from RIKEN Bio Resource Center
(http://www.brc.riken.go.jp/lab/epd/Eng/index.html). The database
of Physcomitrella EST clones is available at the PHYSCODbase
(http://moss.nibb.ac.jp).

FEATURES
    source
        Location/Qualifiers
            1..650
                /organism="Physcomitrella patens subsp. patens"
                /mol_type="mRNA"
                /sub_species="patens"
                /db_xref="taxon:145481"
                /clone="pPhn25113"
                /tissue_type="mixture of chloronemata, caulonemata and
                rhizoid-like protonemata"
                /clone_lib="normalized full length cDNA library,
                chloronemata, caulonemata and rhizoid-like protonemata"

ORIGIN
Alignment Scores:
Pred. No.: 3,616-115 Length: 650
Score: 974.00 Matches: 186
Percent Similarity: 98.96% Conservative: 4
Best Local Similarity: 96.88% Mismatches: 2
Query Match: 97.60% Indels: 0
Gaps: 3
DB: 3

US-10-688-481-11 (1-192) x BU599136 (1-650)

Qy 1 MetPheLeuValAapTTPheTYGlyPheLeuAAserIlegIleuTTPGlnLysGlu 20
Db 603 ATGTTTATCGTAGATTGCTTTATAGCTTCTTCGAGCAATAGCTTGTGCAAGAGAG 544
Qy 21 AlAlaValIleLeuPheLeuGlyLeuAspAsnAAGlyLeuThrThrLeuLeuHISMetLeu 40

```


RESULT 4

Bj609449/c

LOCUS Bj609449/c 740 bp mRNA linear EST 22-OCT-2003

DEFINITION B5f09449 normalized full length cDNA library, chloronemata, caulonema and rhizoid-like protonemata Physcomitrella patens subsp.

ACCESSION B5f09449

VERSION B5f09449

KEYWORDS B5f09449 GI:37851441

SOURCE EST.

ORGANISM Physcomitrella patens subsp. patens
Physcomitrella patens subsp. patens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
1 (bases 1 to 740)
Nishiyama,T., Fujita,T., Shin-i,T., Seki,M., Nishide,H.,
Kohara,Y., Kamaya,A., Carninci,P., Hayashizaki,Y., Shinozaki,K.,
Uchiyama,Y. et al. Comparative genomics of Physcomitrella patens gametophytic
transcriptome and Arabidopsis thaliana: implication for land plant
evolution
Proc. Natl. Acad. Sci. U.S.A. 100 (13), 8007-8012 (2003)

TITLE 12808149

JOURNAL Contact: Tadasu Shin-i
PUBMED Center For Genetic Resource Information
COMMENT National Institute of Genetics
111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel.: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp
A backbone of the vector is basically from pBluescript II (KS),
that was in vivo excised from a 1-Fic phase vector (Carninci et al.,
2001). 5' end of the cDNA that was digested with XhoI was ligated
to SalI site of the vector and the 3' end including polyA tail was
ligated to BamHI site of the
vector(5'- ggaagaaagaagatccacacctgagagattttttttttttaa-3' was
used as a 1st 3' primer, and
5'-gtgttcgcagtcatcgtctgtccagacaagagatgactcgaaaccgannnn-3' as 2nd
5'-hairpin primer, giving the following 5' boarder sequence,
AGGCGAAATGGCCGACTCGCAATTCGTCAAGACC). cDNA insert could be
amplified with conventional T7 and T3 primers. This full-length
cDNA library was generated according to the method described in
Nishiyama et al. (2003).
Protonemata were blended by the POLYTRON, and then cultivated on
the BCDMG medium for 13- 14 days under the continuous light.
These clones are available from RIKEN Bio Resource Center
(http://www.brc.riken.go.jp/lab/spd/Eng/index.html). The database
of Physcomitrella EST clones is available at the PHYSCOBASE
(http://mes.nibb.ac.jp).

FEATURES

SOURCE location/Qualifiers

1..740

/organism="Physcomitrella patens subsp. patens"

/mol_type="mRNA"

/sub_species="patens"

/db_xref="taxon:145481"

/clone="pphm47g10"

/tissue_type="mixture of chloronemata, caulonemata and
rhizoid-like protonemata"

/clone_1fb="normalized full length cDNA library"

chloronemata, caulonemata and rhizoid-like protonemata"

ALIGNMENT SCORES:

pred. No.:	4,34e-115	length:	740
Score:	974.00	Matches:	186
Percent Similarity:	98.96%	Conservative:	4
Best Local Similarity:	96.88%	Mismatches:	2
Query Match:	97.60%	Indels:	0
DB:	3	Gaps:	0

US-10-688-481-11 (1-192) x Bj609449 (1-740)

ORIGIN

1 MetPheLeuValAlaSerTyrPheArgLysPheLeuAlaSerIleGlyLeuTrpGlnIleValGlu 20

Dp		605	ATGTTTATCGAAGATTGGTTTTATGCTTTTCGCGACGATAGGTTTGTTGGCAAGAAG	546
Oy		21	AlalysylleuPheIeuGlyLeuAspAsnAlaGlyLysThrThrIleuLeuHisMetLeu	40
Dp		545	GCCAAATCTGTGTTCTCGGCTTGAACAATGCCGGGAAGCGAACACTTTCGCATGCTC	486
Oy		41	LysAspGluLysIleuGIglnHisGlnProThrGlnTyfProThrsereGluGluSer	60
Dp		485	AAGATATGAAACCTGGGGCAACATCAACCAACGACAGTATCCAACATCTGAAGAAATTGAC	426
Oy		61	IleAsnArgValLysPheLysAlaPheAspLeuGIglnHsthrlleaLaArgVal	80
Dp		425	ATCATATAGGGGTAAGTTCAAAGCATTCGATCTAGTGSTGCACACGATTGCTCGACGTGTG	366
Oy		81	TTPARGAspTYfTYfTrAlaLysValAspAlaAlaIstValTyfLeuValAspAlaValAspArg	100
Dp		365	TGGAGGACACTACTTGTGCTAAGTGGAGTCACTACTTACCCTTGTGCGACGAGTTGACAAAG	306
Oy		101	GluArgPheAlaGluSerLysLysGluLeuAspserLeuSerLeuSerAspAspserLeuSer	120
Dp		305	GAGAGGTTTCTGTAATCAAGAAAAGAACTGCACTCTTGCTCTCGATGACTGCTTCC	246
Oy		121	GlnValProValIleuValIleuGIglnLysAsnLysIleAspIleProTyfAlaAspSereGluAsp	140
Dp		245	CAATGCTGCTGCTGCTGCTGCTTGGCAACAAGATTGACATCCCTTACCGTGCTCGGAAGAT	186
Oy		141	GluLeuArgPheThrIleuGIglnLeuThrMetThrThrglyLysglyThrValAsnLeuGly	160
Dp		185	GAATTGGCGGTACACACTCGGCTTGACCATGACCCTGGCAAGAGACGGTGAACCTTGAAAG	126
Oy		161	AspSerAsnIleAspProIleGluValPheMetCysSerIleValArgLysMetGlyTyf	180
Dp		125	GATGACCAACATCCGGCCCATTTAGAGTTTCAATGTGACGATAGTGCATAAGATGGGTTTC	66
Oy		181	GlyGluGIglnPheLysTRPmetThrglnTyfIleLys	192
Dp		65	GGCGAAGGTTCAAGTGGATGACCCAGATATTATAA	30
RESULT 5				
LOCUS	B0037417	638 bp	mRNA	linear EST 23-AUG-2002
DEFINITION	94613BP10.y1 946 - tassael primordium prepared by Schmidt lab Zea mays cDNA, mRNA sequence.			
ACCESSION	B0037417			
VERSION	B0037417.1	GI:22472937		
KEYWORDS	EST.			
SOURCE	Zea mays			
ORGANISM	Zea mays			
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.			
AUTHORS	1 (bases 1 to 638)			
TITLE	Maize ESTs from various cDNA libraries sequenced at Stanford University			
JOURNAL	Unpublished (1999)			
COMMENT	Contact: Walbot V Department of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USA Tel.: 650 723 2227 Fax: 650 725 8221 Email: walbot@stanford.edu Plate: 946138 row: F column: 10. Location/Qualifiers 1..638 /organism="Zea mays" /mol_type="mRNA" /cultivar="OH43" /db_xref="taxon:4577" /tissue_type="tassael8" /des_features="just after the transition from vegetative to inflorescence development"			

/lab host="XLOLR"
 /clone_lib="946 - tassal primordium prepared by Schmidt
 /note="Organ: tassals, Vector: HybridAP; Site 1: EcorI;
 Site 2: XhoI; George Chuck dissected immature tassals
 between 1mm and 3mm. Sharon Stanfield prepared the cDNA
 library in HybridAP. Sample insert size range was 350 bp
 to 3 Kb with a 1 Kb average."

ORIGIN

Alignment Scores:

Pred. No.: 4,51e-103 Length: 638
 Score: 880.50 Matches: 163
 Percent Similarity: 94.30% Conservative: 19
 Best Local Similarity: 84.46% Mismatches: 10
 Query Match: 88.23% Indels: 1
 DB: 5 Gaps: 1

US-10-688-481-11 (1-192) x BU037417 (1-638)

Qy 1 MetPheLeuValAspTrpPheTyrGlyPheLeuAlaSerIleGlyLeuTrpGlnLeu 20
 Db 41 ATGTTCTGCTGACCTGCTCTGACACGCGGCAAGACCTCTCCACATGCTG 100
 Qy 21 AlAlaValIleLeuPheLeuGlyLeuAspAsnAlaGlyLeuThrLeuLeuHisMetLeu 40
 Db 101 GCTAAGATCTCTCTCTGCTGCTGACACGCGGCAAGACCTCTCCACATGCTG 160
 Qy 41 LysAspGluLeuLeuGlyGlnHisGlnProThrGlnTyrProThrSerGluGluLeuSer 60
 Db 161 AAGGACGAGCGGCTCGTACACGACCGACCGAATCCCACTGACAGAGGTTGAGC 220
 Qy 61 IleAsnArgValIleAspPheValIleAspPheLeuGlyGlyHisThrIleAlaArgVal 80
 Db 221 ATCGGACGATCAAGTTCAGAGCGCTTGCAGCTTGGCGGCAACAGATCGCCCGCGTC 280
 Qy 81 TrpArgAspTyrTyrAlaLeuValAspAlaIleValTyrLeuValAspAlaValAspArg 100
 Db 281 TGGAGGACTACTACGCGCAAGGTTGATGCTGTGTGACTGTGGATGCTGTGACAG 340
 Qy 101 GluArgPheAlaGluSerIleValGlyLeuAspSerLeuSerLeuSer 120
 Db 341 GAACGTTTCCGACGTCGAAAGAGAGACTGACGCTTCTTGACATGACTCCCTTGC 400
 Qy 121 GlnValProValLeuValIleGlyAsnLysIleAspIleProTyrAlaSerSerGluAsp 140
 Db 401 AACGTTCTTCTCTCATACGCGCAACAGATTGACATCCATACGCGGCTTGCAGAGAG 460
 Qy 141 GluLeuArgPheThrLeuGlyLeuThr---MetThrThrGlyGlyGlyThrValAsnLeu 159
 Db 461 GAGCTGAGTACTACCTCGGCTCGGACCACTTCAACCGGGAAGGCAACGTAACCTTG 520
 Qy 160 GluAspSerAsnIleArgProIleGlnValPheMetCysSerIleValArgLysMetGly 179
 Db 521 GCCGACTCCAACTGCGCGGCTTGCAGATCTTCAATGTCAGATGTCGCGCAAGATGGC 580
 Qy 180 TyrGlyGlnGlyPheLeuTyrMetThrGlnTyrIleLys 192
 Db 581 TATGCGAAGGCTTCAATGATGTCACGATCAAG 619

RESULT 6

BU098049 669 bp mRNA linear EST 29-AUG-2002
 LOCUS BU098049 946123E11.y1 946 - tassal primordium prepared by Schmidt lab Zea
 DEFINITION may's cDNA, mRNA sequence.
 ACCESSION BU098049
 VERSION BU098049.1 GI:22545690
 KEYWORDS EST.
 ORGANISM Zea mays

Zeae
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 669)
 AUTHORS Walbot V.
 TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
 JOURNAL Unpublished (1999)
 COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 946123 row: E column: 11.
 Location/Qualifiers

FEATURES

Source

1..669
 /organism="Zea mays"
 /mol_type="mRNA"
 /cultiivar="OH43"
 /db_xref="taxon:4577"
 /issue_type="tassals"
 /dev_stage="just after the transition from vegetative to
 inflorescence development"
 /lab_host="XLOLR"
 /clone_lib="946 - tassal primordium prepared by Schmidt
 lab"
 /note="Organ: tassals, Vector: HybridAP; Site 1: EcorI;
 Site 2: XhoI; George Chuck dissected immature tassals
 between 1mm and 3mm. Sharon Stanfield prepared the cDNA
 library in HybridAP. Sample insert size range was 350 bp
 to 3 Kb with a 1 Kb average."

ORIGIN

Alignment Scores:

Pred. No.: 4.83e-103 Length: 669
 Score: 880.50 Matches: 163
 Percent Similarity: 94.30% Conservative: 19
 Best Local Similarity: 84.46% Mismatches: 10
 Query Match: 88.23% Indels: 1
 DB: 5 Gaps: 1

US-10-688-481-11 (1-192) x BU098049 (1-669)

Qy 1 MetPheLeuValAspTrpPheTyrGlyPheLeuAlaSerIleGlyLeuTrpGlnLeu 20
 Db 1 ATGTTCTGCTGACCTGCTCTGACACGCGGCAAGACCTCTCCACATGCTG 60
 Qy 21 AlAlaValIleLeuPheLeuGlyLeuAspAsnAlaGlyLeuThrLeuLeuHisMetLeu 40
 Db 61 GCTAAGATCTCTCTCTGCTGCTGACACGCGGCAAGACCTCTCCACATGCTG 120
 Qy 41 LysAspGluLeuLeuGlyGlnHisGlnProThrGlnTyrProThrSerGluGluLeuSer 60
 Db 121 AAGGACGAGCGGCTCGTACACGACCGACCGAATCCCACTGACAGAGGTTGAGC 180
 Qy 61 IleAsnArgValIleAspPheValIleAspPheLeuGlyGlyHisThrIleAlaArgVal 80
 Db 181 ATCGGACGATCAAGTTCAGAGCGCTTGCAGCTTGGCGGCAACAGATCGCCCGGTC 240
 Qy 81 TrpArgAspTyrTyrAlaLeuValAspAlaIleValTyrLeuValAspAlaValAspArg 100
 Db 241 TGGAGGACTACTACGCGCAAGGTTGATGCTGTGTGACTGTGGATGCTGTGACAG 300
 Qy 101 GluArgPheAlaGluSerIleValGlyLeuAspSerLeuSerLeuSerLeuSer 120
 Db 301 GAACGTTTCCGACGTCGAAAGAGAGACTGACGCTTCTTGACATGACTCCCTTGC 360
 Qy 121 GlnValProValLeuValIleGlyAsnLysIleAspIleProTyrAlaSerSerGluAsp 140
 Db 361 AACGTTCTTCTCTCATACGCGCAACAGATTGACATCCATACGCGGCTTGCAGAGAG 420
 Qy 141 GluLeuArgPheThrLeuGlyLeuThr---MetThrThrGlyGlyGlyThrValAsnLeu 159
 Db 421 GAGCTGAGTACTACTCGGCTCGGACCACTTCAACCGGGAAGGCAACGTAACCTTG 480

Qy 160 GlyaSpSeranilearProileGluValPheMetCysSerileValArgLysMetGly 179
 Db 481 GCCGACTCCAAAGCCCGCCCTGAGATCTTCATGTGCAATGTCGCGCAAGATGGC 540
 Qy 180 TyrGlyGluGlyPheMetThrGlnTyrIleLeu 192
 Db 541 TATGGCGAAGGCTTCAATGATGTCTCAGTACATCAAG 579

RESULT 7
 LOCUS COS26683 720 bp mRNA linear EST 15-JUN-2004
 DEFINITION 3530_1_177_1.E04.y.1.3530 - Full length cDNA library created by
 INVITROGEN from multiple tissues Zea mays cDNA, mRNA sequence.
 ACCESSION COS26683
 VERSION COS26683.1 GI:50331557
 KEYWORDS EST.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 720)
 Maiboc V.
 Maize ESTs from various cDNA libraries sequenced at Stanford
 University
 Unpublished (1999)
 CONTACT: Maiboc V.
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: maiboc@stanford.edu
 Plate: 3530.1.177.1 row: E column: 04.
 Location/Qualifiers
 1..720
 /organism="Zea mays"
 /mol_type="mRNA"
 /cultivar="B73"
 /db_xref="taxon:4577"
 /tissue_type="multiple"
 /dev_stage="varies by tissue"
 /lab_host="DH10B"
 /clone_id="3530 - Full length cDNA library created by
 INVITROGEN from multiple tissues"
 /note="Organ: silks, husks, ears, pollen, shoot tips,
 leaf, root tips, whole seed, embryo; Vector: pCMV-SPORT
 6.1; Site_1: Bcory; Site_2: NotI; Maize Gene Discovery
 Project contracted with INVITROGEN to produce a
 normalized, full length library in a pSPORT vector. This
 is a Gateway compatible vector, permitting clone movement
 to new vector backbones for expression in diverse host
 cells using recombination rather than restriction enzymes.
 Details of the vector and sequencing primers are available
 at ZMDB in the EST library description tables. poly(A)+
 mRNA was prepared by INVITROGEN, and equimolar amounts of
 RNA from each of the 12 tissue samples were mixed together
 for selection of mRNA with a 5' cap. After synthesis of
 cDNA, a normalization step was conducted against the
 mixture of RNA sources. This step effected a 20X to 80X
 reduction in common transcript types. Tissues prepared: 1.
 just emerging silks; 2. inner husks from ears of sample
 #1; 3. 20 day aleurone; 4. immature tassels, stages from
 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm
 vegetative shoot tips from 15 day old seedlings; all
 leaves with an expanded or partially expanded sheath
 were removed; 8. mature leaf tissue; 9. 0.5 cm long root
 tips from 15 day old seedlings; 10. 10 day whole seed; 11.
 12 day endosperm and embryo; 12. 17 day endosperm and
 embryo. All of the sequenced clones in project 3530 will
 be archived at the University of Arizona along with the
 unique clones from the Maize Gene Discovery EST

ORIGIN
 Alignment Scores:
 Pred. No.: 5,36e-103 Length: 720
 Score: 880.50 Matches: 163
 Percent Similarity: 94.30% Conservative: 19
 Best Local Similarity: 84.46% Mismatches: 10
 Query Match: 88.23% Indels: 1
 DB: 7 Gaps: 1

US-10-688-481-11 (1-192) x COS26683 (1-720)

Qy 1 MetPheLeuValAspTrpPheTyrGlyPheLeuAlaSerileGlyLeuTrpGlnLysGlu 20
 Db 100 ATTTCTCTGTGACTGTGTTCTATGGGGTCTGACATCGCTTGTCGTCAGAAAGAG 159
 Qy 21 AlaLysileuPheLeuGlyLeuAspAsnAlaGlyLysThrThrLeuLeuHismetLeu 40
 Db 160 GCTAAGATCTCTTCTTGTGCTCGACCAAGCGGGAAGCAACCTCTCCACATGCTG 219
 Qy 41 LysAspGluLysLeuGlyGlnHisGlnProThrGlnTyrProThrSerGluLeuSer 60
 Db 220 AAGGACGAGCGGCTCGTACAGCACCAAGCCACAGTACCCACGTCAGAAAGTTGAGC 279
 Qy 61 IleAsnArgValLysPheLysAlaPheAspLeuGlyGlyHisThrIleAlaArgArgVal 80
 Db 280 ATCGGCGAGTCAAGATTCAAGGGCGTTGACTGGGGGCCCAAGATCGCCCGCGTTC 339
 Qy 81 TrpArgAspTyrTyrAlaLysValAspAlaIleValTyrLeuValAspAlaValAspArg 100
 Db 340 TGGAAAGACTACACCGCAAGCTTGATGCTGTGTGACTGATGATGATGATGATGATG 339
 Qy 101 GluArgPheAlaGluSerLysLysGluLeuAspSerLeuLeuSerLeuSer 120
 Db 400 GAACGTTTCCGAGTCGAAGAAAGAGCTTGATGCGCTTCTCAGATGACTCCCTTGCA 459
 Qy 121 GlnValProValLeuValLeuGlyAsnLeuIleAspIleProTyrAlaSerSerGluAsp 140
 Db 460 AACGTTCTTCTCTCACTCGGCGCAACAGATTGACTCCATACGCGGCTTCAGAGAG 519
 Qy 141 GluLeuArgPheThrLeuGlyLeuThr--MetThrThrGlyLysGlyThrValAsnLeu 159
 Db 520 GAGCTGAGTACACTCTCGGCTCGAGCACTTCACAAACCGGAAGCAACGTGAATTG 579
 Qy 160 GlyaSpSeranilearProileGluValPheMetCysSerileValArgLysMetGly 179
 Db 580 GCCGACTCCAAAGCCCGCCCTGAGATCTTCATGTGCAATGTCGCGCAAGATGGC 639
 Qy 180 TyrGlyGluGlyPheMetThrGlnTyrIleLeu 192
 Db 640 TATGGCGAAGGCTTCAATGATGTCTCAGTACATCAAG 678

RESULT 8
 LOCUS B0779008 724 bp mRNA linear EST 26-JUN-2002
 DEFINITION 946116C06.y1.946 - tassels primordium prepared by Schmidt lab Zea
 mays cDNA, mRNA sequence.
 ACCESSION B0779008
 VERSION B0779008.1 GI:21987480
 KEYWORDS EST.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 724)
 Maiboc V.
 Maize ESTs from various cDNA libraries sequenced at Stanford


```

Db      417 GAAAGATTTCAGATGCAAGAAAGAGTGGATGCTCTCTCTCTGATGAGTCCCTGCC 358
        |||
Qy      121 GlnValProValLeuValLeuGlyAsnLysIleAplIleProTyrAlaSerSerGluAsp 140
        |||
Db      357 AATGATCTTTCTTGATTTGGCAATAGATGACATCCATGCTGCTTCTGAAGAT 298
        |||
Qy      141 GluLeuArgPheThrLeuGlyLeuThr---MetThrThrGlyLysGlyThrValAsnLeu 159
        |||
Db      297 GAAATGGCGTTACCAATGGGGTTGACAGGCATCAACCTGCAAGGAAAGGTGAACCTG 238
        |||
Qy      160 GlyAspSerAsnIleArgProIleGluValAlaPheMetCysSerIleValArgLysMetGly 179
        |||
Db      237 GCAGATTCCAATGTTCCCTCTCGAGGATTCATGTCGACATAGTCCGCAAGATGGCT 178
        |||
Qy      180 TyrGlyGluGlyPheLysTyrMetThrGlnTyrIleLys 192
        |||
Db      177 TATGGAAGAGGCTTCAATGATGTCTCAATACATTAAG 139

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RESULT 10
DR829325      830 bp      mRNA      linear      EST 28-JUL-2005
LOCUS        ZM_BF0075D10.r_ZM_BfB_Zea_mays cDNA 5', mRNA sequence.
DEFINITION   DR829325
ACCESSION    DR829325.1 GI:71448275
VERSION      EST.
KEYWORDS     Zea mays
SOURCE       Zea mays
ORGANISM     Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
              clade; Panicoideae; Andropogoneae; Zea.
REFERENCE    1 (bases 1 to 830)
AUTHORS      Kim,H., Collier,K., Wisotscki,M., Smart,D., Kudrna,D., Muller,C.,
              Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu,Y.
TITLE        Maize Full-length cDNA Project
JOURNAL      Unpublished (2005)
COMMENT      Contact: Yeisoo Yu
              Arizona Genomics Institute
              The University of Arizona
              Forbes Building Room 303, Tucson, AZ 85721-0036, USA
              Tel: 520 626 9585
              Fax: 520 621 1259
              Email: yeisoo@genome.arizona.edu
              Plate: 0075 row: D column: 10.
              Location/Qualifiers
                1..830
                /organism="Zea mays"
                /mol_type="mRNA"
                /culivar="B73"
                /db_xref="taxon:4577"
                /tissue_type="mixed (silks, husks, ears, pollen, shoot
                tips, leaf, root tips, whole seed, embryo)"
                /dev_stage="varies by tissue"
                /lab_host="DH10B T1 phage resistant"
                /clone_lib="ZM_BfB"
                /note="Vector: pCMV-SPORT 6.1; Site_1: EcoRV; Site_2:
                NotI; Maize Full length cDNA library (3510 library)
                created by invitrogen from multiple tissues; Organ: silks,
                husks, ears, pollen, shoot tips, leaf, root tips, whole
                seed, embryo. This is a Gateway compatible vector,
                permitting clone movement to new vector backbones for
                expression in diverse host cells using recombination
                rather than restriction enzymes. poly(A)+ mRNA was
                prepared by invitrogen, and equimolar amounts of RNA from
                each of the 12 tissue samples were mixed together for
                selection of mRNA with a 5' cap. After synthesis of cDNA,
                a normalization step was conducted against the mixture of
                RNA sources. Tissues prepared: 1. just emerging silks; 2.
                inner husks from ears of sample #1; 3. 20 dap aleurone; 4.
                immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to
                2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from
                15 day old seedlings; all leaves with an expanded or
                partially expanded sheath were removed; 8. mature leaf

```

tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in Maize Full-length cDNA Project will be archived at the University of Arizona. Clones, high density filters and amplified library can be ordered from the University of Arizona (<http://www.genome.arizona.edu/orders/>).

ORIGIN

Alignment Scores:

Pred. No.:	Length:	Score:	Matches:	Conservative:	Percent Similarity:	Best Local Similarity:	Mismatches:	Query Match:	Indels:	Gaps:
6,55e-103	830	880.50	163	19	94.30%	84.46%	10	88.23%	1	

US-10-688-481-11 (1-192) x DR829325 (1-830)

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Qy      1 MetPheLeuValAlaPheTyrPheTyrGlyPheLeuAlaSerIleGlyLeuTyrGlnLysGlu 20
        |||
Db      128 ATGTTCTCTGTGACCTGCTTCTATGGGGTGTGTCGATCGCTTGCGCTGTGGCAAGAGAG 187
        |||
Qy      21 AlaValIleLeuPheLeuGlyLeuAspAsnAlaGlyLysThrThrLeuLeuHisMetLeu 40
        |||
Db      188 GCTAAGATCCTCTTCTCTGCTGCGACGACGCGGCAAGCACCTCTCTCCATGCTG 247
        |||
Qy      41 LysAspGluLysLeuGlyGlnHisGlnProThrGlnTyrProThrSerGlnLysLeuSer 60
        |||
Db      248 AAGGAGAGAGGGCTCGTAGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 307
        |||
Qy      61 IleAsnArgValLysPheLysAlaPheAspLeuGlyGlyHisThrIleAlaArgVal 80
        |||
Db      308 ATCGGCGAGATCAAGTTCAGAGGGCTTCGACCTTGGGGGCCACCAAGATCGCCCGCGTC 367
        |||
Qy      81 TrpArgAspTyrTyrAlaLysValAlaPheAlaIleValTyrLeuValAlaPheArg 100
        |||
Db      368 TGGAGGACTACACAGGCAAGGTTGATGCTGTGTGATCTTGATGCTGTGACAG 427
        |||
Qy      101 GluArgPheAlaGluSerLysGluLeuAspSerLeuSerAspAspSerLeuSer 130
        |||
Db      428 GAACGTTTCCGAGTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 487
        |||
Qy      121 GlnValProValLeuValLeuGlyAsnLysIleAplIleProTyrAlaSerSerGluAsp 140
        |||
Db      488 AACGTTCTTCTCTCATCTGCGCAACAGATTGACATCCCATACGCGCTTCAGAGAGAG 547
        |||
Qy      141 GluLeuArgPheThrLeuGlyLeuThr---MetThrThrGlyLysGlyThrValAsnLeu 159
        |||
Db      548 GAGCTGAGTACTACTCTCGGCTGAGCACTTCAACAACGGAGAGAGAGAGAGAGAGAGAGAG 607
        |||
Qy      160 GlyAspSerAsnIleArgProIleGluValAlaPheMetCysSerIleValArgLysMetGly 179
        |||
Db      608 GCGGATCTCCATGTCGCGCCCTCGAGATCTTCATGTCAGTGTGTGTGCGCAAGATGGC 667
        |||
Qy      180 TyrGlyGluGlyPheLysTyrMetThrGlnTyrIleLys 192
        |||
Db      668 TATGGAAGAGGCTTCAATGATGTCTCAATACATTAAG 706

```

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RESULT 11
DR824574      877 bp      mRNA      linear      EST 28-JUL-2005
LOCUS        ZM_BF0066H23.r_ZM_BfB_Zea_mays cDNA 5', mRNA sequence.
DEFINITION   DR824574
ACCESSION    DR824574
VERSION      DR824574.1 GI:71443524
KEYWORDS     Zea mays
SOURCE       Zea mays
ORGANISM     Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
              clade; Panicoideae; Andropogoneae; Zea.
REFERENCE    1 (bases 1 to 877)

```

AUTHORS Kim, H., Collura, K., Wisotski, M., Smart, D., Kudrna, D., Muller, C., Rao, K., Haller, K., Wang, R., Soderlund, C., Walbot, V. and Yu, Y.

TITLE Maize full-length cDNA Project

JOURNAL Unpublished (2005)

COMMENT Contact: Yeisoo Yu
Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9585
Fax: 520 621 1259
Email: yeisoo@genome.arizona.edu
Plate: 0066 row: H column: 23.
Location/Qualifiers

FEATURES

source

1. 877
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="B73"
/db_xref="taxon:4577"
/tissue_type="mixed (silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo)"
/dev_stage="varies by tissue"
/lab_host="DH10B T1 phage resistant"
/clone_id="ZM_BFB"
/note="Vector: PCMV-SPORT 6.1, Site 1: EcoRV, Site 2: NotI; Maize full length cDNA library (3530 library) created by Invitrogen from multiple tissues: Organ: silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo. This is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. poly(A) + mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. immature tassels; 5. stamens from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in Maize full-length cDNA Project will be archived at the University of Arizona. Clones, high density filters and amplified library can be ordered from the University of Arizona
(http://www.genome.arizona.edu/orders/)."

ORIGIN

Alignment Scores:

Pred. No.: 7.08e-103 Length: 877
Score: 880.50 Matches: 163
Percent Similarity: 94.30% Conservative: 19
Best Local Similarity: 84.46% Mismatches: 10
Query Match: 88.23% Indels: 1
DB: 8 Gaps: 1

US-10-688-481-11 (1-192) x DR824574 (1-877)

QY 1 MecheleuValAapTTPPhetYrGlyPheleuAlaserlleglyLeutTPGlnlyGlu 20
Db 128 ATGTTCTGTGGAGCTGTTCTATGCGGTCTGTCATCGCTGGCTGTGGCAAGAG 187
QY 21 AlatyrlleuPheleuGlyLeuAspAsnAlaglylyrThrTrlleuLeuHleMetleu 40
Db 188 GCTAAGATCTCTTCTTGGCTCGACAAACCCGCAAGACCACTCTCTCCATGCTG 247
QY 41 LysApGlyuLyLeuGlyGlnHleGlnProThrGlnTyProThrIserGluGluLeuSer 60
Db 248 AAGAGCGAGCGGCTCGTACAGACACAGCGAGAGTACCCCACTGAGAAAGTTGAGC 307

QY 61 lIeasArVallybshelysAlapheAspleuGlyHleThrllleAlarGArVal 80
Db 308 ATGGGAGATCATAGTTCAAGGGCTTCGACTTGGGGGACACAGATCCGCCGCCGTC 367
QY 81 TTPAAGAsPTyTYrAlalyeValapAlleValTyTrlleuValAspAlaValAapAg 100
Db 368 TGGAGAGTACTTACCCCAAGGTTGATGCTGTGTACTTGGTGAATCTGTTCAGAG 427
QY 101 GUArGPhelAgluserlyslsGluLeuAspSerLeuSerAspAspSerLeuSer 120
Db 428 GAACGTTTGGAGCTCGAGTCAAGAGAGGCTTGATGCTCTTGCAGATATCTCTTCCA 487
QY 121 GlnAlProValleuValleuGlyAsnlysleAspIleProTyAlaserGluAap 140
Db 488 AACGTTCTTCTCTCATCTGCGCAACAGATTCATCCATACCGCGCTTCAGAGAG 547
QY 141 GluleuArGPhetThrleuGlyleuThr--MetThrThGlylyslsThrValanleu 159
Db 548 GAGCTGAGGTACTTACTCTCGCTGAGCACTTCACAAACCGGAGGCAACGGAACCTTG 607
QY 160 GlyAspSerAsnleArProIleGluValPheMetCysSerlleValArGlyMetGly 179
Db 608 GCCGACTCCAAATGTCGGCCCTCGAGATCTTCATATGCAATGTGTGGTCAAGATGGC 667
QY 180 TyGlyGlyGlyPheTyStrMetThrGlnTyrllelye 192
Db 668 TATGGGAGAGGCTTCAATGAGATGTCTCATGATCATCAAG 706

RESULT 12

CO443833 903 bp mRNA linear EST 08-JUN-2005
LOCUS MZCCL10063007.5 Maize Endosperm cDNA Library Zea mays cDNA, mRNA
DEFINITION sequence.

ACCESSION CO443833
VERSION CO443833.1 GI:67015084
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S., Fiech, P.H., De Rosa, V.E., Jr., Martins, M.M., Vettore, A.L., da Silva, F.R. and Arruda, P.
Endosperm-preferred expression of maize genes as revealed by transcriptome-wide analysis of expressed sequence tags
Plant Mol. Biol. (2005) In press

TITLE

JOURNAL
COMMENT Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: patricia@unicamp.br.

FEATURES

source

1. 903
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="F-352 near isogenic line"
/db_xref="taxon:4577"
/sex="thermaphrodite"
/tissue_type="endosperm"
/dev_stage="multiple stages (10 to 25 days after pollination, see publication for more information)"
/lab_host="E. coli DH10B"
/clone_id="Maize Endosperm cDNA Library"
/note="Organ: seed. Vector: pSPORT1. Site 1: SalI. Site 2: NotI; Plant Material and RNA Isolation: Field grown maize plants from inbred line F352 were used. Ears were harvested at 10, 15, 20 and 25 days after pollination (DAP). Seeds were cut from the ear and the upper third of the endosperm, containing only endosperm, aleurone and

pericarpal tissues, was removed, frozen in liquid nitrogen and stored at -800 C. Frozen endosperms were pulverized in liquid nitrogen and total RNA was isolated according to the method of Manning (9). Poly(A)+RNA was isolated using Oligotex-dT. cDNA libraries were constructed using Superscript Plasmid System for cDNA Synthesis and Plasmid Cloning Kit as described in Vectors, et al., (2001). The libraries that made SUCSEST. Genet Mol Biol 24: 1-7. cDNAs ranging from 500 to 800 bp in size were assigned as short libraries (S10, S15, S20), and cDNAs >800 were assigned as long libraries (L10, L15, M15, M20, L25). Unamplified libraries were plated and individual colonies picked and transferred to 96 well plates containing liquid Circle Grow (CG) medium supplemented with 100 mg/L of ampicillin and 8% glycerol. Three copies of each cDNA clone were stored at -800 C. Additional information can be found in : Verra, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S., Flech, P.H., De Rosa Jr., V.E., Martins, M.M., Vettore, A.L., da Silva, F.R. and Arruda, P. (2005) Endosperm-preferred expression of maize genes as revealed by transcriptome-wide analysis of expressed sequence tags. Plant Molecular Biology (/in press/)"

ORIGIN

Alignment Scores:
Pred. No.: 7.37e-103 Length: 903
Score: 880.50 Matches: 163
Percent Similarity: 94.30% Conservative: 19
Best Local Similarity: 84.46% Mismatches: 10
Query Match: 88.23% Indels: 1
Gaps: 1

US-10-688-481-11 (1-192) x CO443833 (1-903)

Qy 1 MetPheUValAspTrpPheTyrGlyPheUValSerIleGlyLeuTrpGlnTyrGlu 20
Db 124 ATGTTCTGGTGGATGAGTCTATGGGGTGTGGGATCGCTTGGCTGTGGCAAGAG 183
Qy 21 AAlaValIleUValPheUValGlyUValAspAlaGlyTyrThrLeuLeuHisMetLeu 40
Db 184 GCTAAGATCCTCTTCTTGGCTCGACACACCCGGCAAGACACCTCTCTCAATGCTG 243
Qy 41 LysAspGlyUValSerIleGlnHisGlnProThrGlnTyrProThrSerGlnUValSer 60
Db 244 AAGGCGAGCGGCTGTGTACACACACGCGACGATGCCACGTCAGAAAGATTAGC 303
Qy 61 IleAsnArgValIlePheUValPheAspLeuGlyGlyHisThrIleAlaArgVal 80
Db 304 ATGGCAGGATCAAGTTCAAGCGCTTGGGGGCGCACAGATGCCCGCGCGCTC 363
Qy 81 TrpArgAspTyrTyrAlaValAspAlaIleValTyrLeuValAspAlaValAspArg 100
Db 364 TGGAAAGCATCTACGCAAGGTTGATCTGTGTGCTTGGTGGATGCTGTGGACAG 423
Qy 101 GluArgPheAlaGlySerIleUValSerIleUValSerIleUValSerIleUValSer 120
Db 424 GAACGTTTGGCGAGTCAGAAAGAGCGCTTCGATGCGCTTTCGAGATGCTCCCTGCA 483
Qy 121 GlnValProValIleUValLeuGlyValSerIlePheProTyrAlaSerSerGluAsp 140
Db 484 AACGTTCTTCTCTACTGTGGCAAGATGATCCATTCATGCTGCTTCAAGAGAG 543
Qy 141 GluLeuArgPheThrLeuGlyLeuThr---MetThrTrpGlyTyrGlyTyrValAsnLeu 159
Db 544 GAGCTGAGGATCTACTGCGCTGAGCAATTCACACCGGGAAGGCAAGTGAATCTG 603
Qy 160 GlyAspSerAsnIleArgProIleGluValPheMetCysSerIleValArgUlyMetGly 179
Db 604 GCCGACTCAACGTCGCGCCCTGGAAGATCTTCATGTGCAAGTGTGTCGCAAGATGGC 663
Qy 180 TyrGlyGlyUValPheUValTrpMetThrGlnTyrIleVal 192
Db 664 TATGGCAAGGCTTCAATGATGTCTCATGATCATCAAG 702

RESULT 13

AY106333

LOCUS

DEFINITION

AY106333

KEYWORDS

ORGANISM

SOURCE

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

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AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

location/Qualifiers

1..1098

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/db_xref="taxon:4577"

/clone_lib="Maize Mapping Project/Dupont Consensus Library"

/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed Dupont contigs; this resource was assembled by Dupont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

ORIGIN

Alignment Scores:

Pred. No.: 9.72e-103 Length: 1098
Score: 880.50 Matches: 163
Percent Similarity: 94.30% Conservative: 19
Best Local Similarity: 84.46% Mismatches: 10
Query Match: 88.23% Indels: 1
Gaps: 1

US-10-688-481-11 (1-192) x AY106333 (1-1098)

Qy 1 MetPheUValAspTrpPheTyrGlyPheUValSerIleGlyLeuTrpGlnTyrGlu 20
Db 189 ATGTTCTGGTGGATGAGTCTATGGGGTGTGGGATCGCTTGGCTGTGGCAAGAG 248
Qy 21 AAlaValIleUValPheUValGlyUValAspAlaGlyTyrThrLeuLeuHisMetLeu 40

Db 249 GCTAAGATCTCTTCTTGCCCTGACCAACCGGCAAGAACCTCTTCACATGCTG 308
 Qy 41 LysAspGluLysLeuGlyGlnHISGlnProThrGlnTyrProThrSerGluLeuSer 60
 Db 309 AAGGACGAGGCGCTCGTACAGCACACGACCAAGACGATCCAGTCAAGAGTTGAGC 368
 Qy 61 LLeAsnArgValLysPheLysAlaPheAspLeuGlyGlnHISThrIleAlaArgVal 80
 Db 369 ATGGGACGATCAAGATTCAAGGGCTTCGACTGGGGGCCACCAAGATCGCCCGCTC 428
 Qy 81 TTPArgAspTyrTyrAlaLysValAspAlaIleValTyrLeuValAspAlaValAspArg 100
 Db 429 TGGAGGACTACTACCGCAAGGTTGATGCTGTGTACTGTGGTGGATGCTGTTCACAG 488
 Qy 101 GlnArgPheAlaGluSerLysGluLeuAspSerLeuSerAspAspSerLeuSer 120
 Db 489 GAACGTTTCCGAGTGAAGAAAGAGACTCGATCGCTTCTTGCAAGTACCTCCCTTGCA 548
 Qy 121 GlnValProValLeuValLeuGlyAsnLysIleAspIleProTyrAlaSerSerGluAsp 140
 Db 549 AAGTTCTCTTCTTCATACCTGGGCAACAGATTGACATCCCATACCGGCTTCAGAGAG 608
 Qy 141 GlnLeuArgPheThrLeuGlyLeuThr--MetThrThrGlyLysGlyThrValAsnLeu 159
 Db 609 GAGCTGAGTACTACTCGGCTGAGCACTTCACACCGGAAAGGCAAGTGAACCTTG 668
 Qy 160 GlnAspSerAsnIleArgProIleGluValPheMetCysSerIleValAlaGlyMetGly 179
 Db 669 GCCGACTCCACAGCTCCGCCCTGGAGATCTTCAATGCAATGATGTCGCCAAGATGGGC 728
 Qy 180 TyrGlyGluGlyPheLysTyrMetThrGlnTyrIleLys 192
 Db 729 TATGGCAAGGCTTCAATGATGTCTCATGATCATCAG 767
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 LOCUS CN206979 861 bp mRNA linear EST 30-APR-2004
 DEFINITION Tort733 Gemetophyte rehydration library Tortula ruralis cDNA, mRNA
 sequence.
 ACCESSION CN206979
 VERSION CN206979.1 GI:46903710
 KEYWORDS EST.
 SOURCE Tortula ruralis
 ORGANISM Tortula ruralis
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
 Bryopsida; Dicranidae; Pottilales; Pottiaceae; Tortula.
 REFERENCE
 AUTHORS Oliver,M.J., Dowd,S.E., Zaragosa,J., Mauget,S.A. and Payton,P.R.
 TITLE The rehydration transcriptome of the desiccation-tolerant bryophyte
 Tortula ruralis: transcript classification and analysis
 JOURNAL BMC Genomics 5 (1), 89 (2004)
 PUBMED 15546486
 COMMENT Contact: Oliver Melvin J
 Plant Stress Lab
 USDA-ARS
 3810 4th St. Lubbock, TX 79415, USA
 Tel: 806-749-5560
 Fax: 806-723-5272
 Email: moliver@ljbk.ars.ueda.gov
 PCR PRIMERS
 FORWARD: GTTTTCCGACTCAGCAGC
 BACKWARD: CAGGAACACGCTATGAC.
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 Location/Qualifiers
 1..861
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 /db_xref="taxon:38588"
 /clone_lib="Gemetophyte rehydration library"
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 Salt; Site_2: NoCl"
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Pred. No.: 8e-103
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 Best Local Similarity: 91.01%
 Query Match: 88.18%
 DB: 7
 Gaps: 0
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 Qy 21 AlAlaValIleLeuPheLeuGlyLeuAspAlaIleValTyrLeuThrThrLeuHISMetLeu 40
 Db 232 GCCAAATTCCTCTTCTGGGCTTCGACCAACGGGGCAAGACACGCTCTTCATATCTC 291
 Qy 41 LysAspGluLysLeuGlyGlnHISGlnProThrGlnTyrProThrSerGluLeuSer 60
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 Qy 61 LLeAsnArgValLysPheLysAlaPheAspLeuGlyGlnHISThrIleAlaArgVal 80
 Db 352 ATCAACAGAGTGAAGTTCAAAAGCTTGTGATTTGGGGGGCACTATCCGCAAGCGCTGTG 411
 Qy 81 TTPArgAspTyrTyrAlaLysValAspAlaIleValTyrLeuValAspAlaValAspArg 100
 Db 412 TGGAGGACTATTATATCCCAAGGTGATGCCATATGCTTACTGATGAGCGCCCTAGACAG 471
 Qy 101 GlnArgPheAlaGluSerLysGluLeuAspSerLeuSerAspAspSerLeuSer 120
 Db 472 GAGAGTTCCAGAGTGAAGAAAGAGCTGAGCTGCTGTGTCTCACAGCACTCTCTCC 521
 Qy 121 GlnValProValLeuValLeuGlyAsnLysIleAspIleProTyrAlaSerSerGluAsp 140
 Db 532 CAAATTCTGTGTACTGTCTGGGAAACCAAGATTGACATCCCGATATCGGCTCTGAGAG 591
 Qy 141 GlnLeuArgPheThrLeuGlyLeuThrMetThrGlyLysGlyThrValAsnLeuGly 160
 Db 592 GAGCTGGATATTCCTTGAGGCTGACCATGACCAAGCCATGAGACCTGTGAACCTGGGC 651
 Qy 161 AspSerAsnIleArgProIleGluValPheMetCysSerIleValAlaGlyMetGlyTyr 180
 Db 652 GACGCAACATCCGGGCCATCGAGTCTTCATGTGCAATATGTGGAAAGATGGGGTAG 711
 Qy 181 GlyGlyGlyPheLysTyrMetThrGln 189
 Db 712 GGAGAAAG-GTCAAGTGAATACGCGT 737
 RESULT 15
 LOCUS DN152566 807 bp mRNA linear EST 16-FEB-2005
 DEFINITION 5207 C08 Fl5 Switchgrass callus cDNA library Panicum virgatum cDNA
 clone 5207_C08_F15 5', mRNA sequence.
 ACCESSION DN152566
 VERSION DN152566.1 GI:59873417
 KEYWORDS EST.
 SOURCE Panicum virgatum (switchgrass)
 ORGANISM Panicum virgatum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Paniceae; Panicum.
 REFERENCE
 AUTHORS Tobias,C.M., Twigg,P., Hayden,D.M., Fladbeck,M.R., Vivian,L.A.,
 Chow,E.K. and Sarach,G.
 TITLE An EST survey of Switchgrass: a C4 perennial grass
 JOURNAL Unpublished (2005)
 COMMENT Contact: Tobias CM
 Genomics and Gene Discovery Unit
 USDA, Agricultural Research Service, Western Regional Research
 Center
 800 Buchanan Street, Albany, CA 94710, USA
 Tel: 510 559-6172

Fax: 510 559-5818
Email: cecobias@w.usda.gov
The piped basecalling program was used to call bases and identify the high scoring region using the '-trim alt' and trim out options. Vector sequences have been removed using the program cross_match.
Seq primer: M13 reverse.
Location/Qualifiers

FEATURES
source

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/mol_type="mRNA"
/cultivar="Kantow"
/db_xref="taxon:38727"
/clone="5207_C08_F15"
/dev_stage="Embryogenic and Nonembryogenic"
/lab_host="E. coli DH5alpha"
/clone_lib="Switchgrass callus cDNA library"
/note="Organ: Callus; Vector: pSPORT1; Site_1: Salt; Site_2: NoCl; Callus was established from mature carpobasis of Switchgrass cv. Kantow and flash frozen in liquid nitrogen. The tissue was cultured by Dan Hayden in the laboratory of CM Tobias. Total RNA and poly(A) RNA were prepared, cDNA synthesized, and directionally ligated into pSPORT1 by Paul Twigg, Biology Department, U. Nebraska Kearney, Kearney, NE. Plasmid DNA preparations and DNA sequencing were performed in the laboratory of CM Tobias."

ORIGIN

Alignment Scores:

Pred. No.: 1.54e-102 Length: 807
Score: 877.50 Matches: 162
Percent Similarity: 94.30% Conservative: 20
Best Local Similarity: 83.94% Mismatches: 10
Query Match: 87.93% Indels: 1
DB: 8 Gaps: 1

US-10-688-481-11 (1-192) x DN152566 (1-807)

QY 1 MetPheLeuValAspTrpPheTyrGlyPheLeuAlaSerIleGlyLeuTrpGlnLeuGlu 20
DB 93 ATGTTCCGTGGTGGACTGTTCTACGGGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG 152
QY 21 AlalysIleLeuPheLeuGlyLeuAspAsnAlaGlyLysThrThrLeuLeuHisMetLeu 40
DB 153 GCCAAGATCTCTCTCGGCTCGACCAACCGCGCAAGACCAACCTCTCCACATGCTC 212
QY 41 LysAspGlyLysLeuGlyGlnHisGlnProThrGlnTyrProThrSerGlnGluLeuSer 60
DB 213 AAGACGACGCGCTCGTACAGCACGCGACGACGACGACGACGACGACGACGACGACGAC 272
QY 61 IleAsnArgValIysPheLysAlaPheAspLeuGlyGlnHisThrIleAlaArgArgVal 80
DB 273 ATCGGCAAGATCAATTCAAGCCCTTCACTCGGCGGCCCAACAGATGCTCGCGCGCTC 332
QY 81 TrpArgAspTyrTyrAlaLysValAspAlaIleValTyrLeuValAspAlaValAspArg 100
DB 333 TCGAAGACTACTACGCAAGGTGATGCTGCGTACTTGTGTGATGCTGTGACACAAG 392
QY 101 GluArgPheAlaGlnSerIleLysGlnLeuAspSerLeuLeuSerAspAspSerLeuSer 120
DB 393 GAACGTTTGGCGATCGAAGAGAGCTGTATGCTCTTCTTTCGACATGACTCACTTGGC 452
QY 121 GluValProValLeuValLeuGlyValAsnLysIleAspIleProTyrAlaSerSerGlnAsp 140
DB 453 AACGTTCTTCTCTCTACTGCGGCAATAAGATTGACATTCGTTACGACGCTTCAGAGAG 512
QY 141 GluLeuArgPheThrLeuGlyLeuThr---MetThrThrGlyLysGlyThrValAsnLeu 159
DB 513 GAGCTGCGGTACTACTCGGCTGAGCAACTTCACACCGGGAAGGCAACGTGAACCTTG 572
QY 160 GlyAspSerAsnIleArgProIleGlnValPheMetCysSerIleValArgLysMetGly 179
DB 573 TCTGACTCAATGTTGCGCCCTCGAAGATCTTCATGTGCAAGTGTGCGCAAGATGGGC 632

QY 180 TyrGlyGlnGlyPheLysTrpMetThrGlnTyrIleLys 192
DB 633 TACGGCAAGGCTTCAATGATGATGCTCAGTACATCAAG 671

Search completed: December 9, 2005, 03:49:44
Job time : 3751 secs

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OM protein - nucleic search, using frame_p2n model

Run on: December 9, 2005, 01:41:52 / Search time 169 Seconds
(without alignments)
2019.478 Million cell updates/sec

Title: US-10-688-481-11
Perfect score: 998
Sequence: 1 MFLVDFYGLASIGLWQKE.....SIVRKMGYGRGFKMTQYIK 192

Scoring table:
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Xgapop 10.0, Ygapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued_Patents_NA:
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	998	100.0	667	3	US-09-828-310-6
2	998	100.0	805	3	US-09-828-310-1
3	674.5	67.6	3191	3	US-09-270-767-13105
4	625	62.6	716	3	US-09-533-559-6898
5	614.5	61.6	724	2	US-08-825-780-2
6	614.5	61.6	1288	3	US-09-149-476-285
7	614.5	61.6	1285	3	US-09-149-476-146
8	585.5	58.7	564	3	US-09-248-796A-6222
9	560.5	56.2	903	3	US-09-016-434-913

10	542	54.3	1700	3	US-09-533-559-125	Sequence 125, App
11	386	38.7	378	3	US-09-621-976-458	Sequence 458, App
12	355	35.6	504	3	US-09-621-976-445	Sequence 445, App
13	306	30.7	271	3	US-09-313-294A-3554	Sequence 3554, App
14	282	28.3	262	3	US-09-016-434-501	Sequence 501, App
15	275.5	27.6	968	3	US-09-949-016-3194	Sequence 3194, App
16	260	26.1	459	3	US-09-270-767-1354	Sequence 1354, App
17	260	26.1	459	3	US-09-270-767-16636	Sequence 16636, A
18	253	25.4	676	3	US-09-533-559-6626	Sequence 6626, App
19	253	25.4	1273	3	US-09-533-559-6704	Sequence 6704, App
20	250.5	25.1	1125	3	US-09-774-528-374	Sequence 374, App
21	250.5	25.1	1125	3	US-10-120-988-374	Sequence 374, App
22	248	24.8	587	3	US-09-513-999C-10983	Sequence 10983, A
23	246	24.6	513	3	US-09-248-796A-6221	Sequence 6221, App
24	245.5	24.6	913	3	US-09-463-339-4	Sequence 4, App1
25	243	24.3	540	3	US-09-621-976-984	Sequence 984, App
26	243	24.3	930	3	US-09-533-559-111	Sequence 111, App
27	242.5	24.3	558	3	US-09-248-796A-6161	Sequence 6161, App
28	241.5	24.2	550	3	US-09-359-301A-24	Sequence 24, App1
29	241.5	24.2	550	3	US-09-771-035A-12	Sequence 12, App1
30	241	24.1	663	3	US-09-533-559-4386	Sequence 4386, App
31	240.5	24.1	3595	3	US-09-949-016-4833	Sequence 4833, App
32	240	24.0	1076	3	US-09-270-767-12090	Sequence 12090, A
33	239	23.9	558	3	US-09-503-391-5	Sequence 5, App1
34	238.5	23.9	536	3	US-08-984-550-3	Sequence 3, App1
35	238.5	23.9	550	3	US-09-359-301A-23	Sequence 23, App1
36	238.5	23.9	550	3	US-09-771-035A-11	Sequence 11, App1
37	238.5	23.9	950	3	US-08-984-550-1	Sequence 1, App1
38	237.5	23.8	1815	3	US-09-220-132-69	Sequence 69, App1
39	237.5	23.8	1855	3	US-09-949-016-2652	Sequence 2652, App
40	237.5	23.8	1985	3	US-09-949-016-2434	Sequence 2434, App
41	237.5	23.8	2366	3	US-09-949-016-2435	Sequence 2435, App
42	235.5	23.6	665	3	US-09-513-999C-3820	Sequence 3820, App
43	234.5	23.5	1005	3	US-09-103-359-4	Sequence 4, App1
44	234	23.4	271	3	US-09-313-294A-3059	Sequence 3059, App
45	234	23.4	543	3	US-09-248-796A-5795	Sequence 5795, App

ALIGNMENTS

RESULT 1
US-09-828-310-6
Sequence 6, Application US/09828310
Patent No. 6689939
GENERAL INFORMATION:
APPLICANT: COSTA E SILVA, OSWALDO DA
APPLICANT: BOHNERT, HANS J.
APPLICANT: VAN THIELEN, NOCHA
APPLICANT: CHEN, ROUYING
TITLE OF INVENTION: GTP BINDING STRESS-RELATED PROTEINS AND METHODS OF USE
FILE REFERENCE: 16313-0039
CURRENT APPLICATION NUMBER: US/09/828,310
CURRENT FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/196,001
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 667
TYPE: DNA
ORGANISM: Physcomitrella patens
US-09-828-310-6
Alignment Scores:
Pred. No.: 5,74e-120
Score: 998.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 3
Gaps: 0
US-10-688-481-11 (1-192) x US-09-828-310-6 (1-667)

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Qy 21 AlAlaValIleLeuPheLeuGlyLeuAspAsnAlaGlyLeuThrThrLeuLeuHisMetLeu 40
Db 93 GCCAAATCCGTGTTCTGGGTCTCGACATGCTGGCAAGACTACTCTTCTGCAATGCTC 152
Qy 41 LysAspGlyLysLeuGlyGlnHisGlnProThrGlnTygProThrSerGlnLysLeuSer 60
Db 153 AAGGATGAGAACTGGGGCAACATCAACCAACGAGTATCCAGCTGACAGAGATTGAGT 212
Qy 61 IleAsnArgValLysPheLysAlaPheAspLeuGlyGlyHisThrIleAlaArgVal 80
Db 213 ATCAACAGATGAGATTCAAGCATTCGATCGGTGGCCACACAACTCGTCGACGGGTG 272
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Db 273 TGGAGGACTACTATGCTTAAGTGATGCTATGATGATCTGCGACGAGTGAACAGG 332
Qy 101 GluArgPheAlaGlySerLysGlyLeuAspSerLeuLeuSerAspAspSerLeuSer 120
Db 333 GAGGATTTCTGATGATCAAGAAAGAGCTCGATTCCTTCTCTCGAGCATTCCTGTCC 392
Qy 121 GlnValProValIleuValIleuGlyAsnLysIleAspIleProTygAlaSerSerGluAsp 140
Db 393 CAAGTTCTGTGCTGCTGCTGGGAAACAAAGATTGATCCGTAAGCTTCTTGAAGAC 452
Qy 141 GluLeuArgPheThrLeuGlyLeuThrMetThrThrGlyGlyThrValAsnLeuGly 160
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Qy 161 AspSerAsnIleArgProIleGlnValPheMetCysSerIleValArgLysMetGlyTyr 180
Db 513 GATACCAACATTCGCGCCATTTGAGGTTTCATGTGCAATATTGTGCGAAATGGGGTAC 572
Qy 181 GlyGlnGlyPheLysTrpMetThrGlnTygIleLys 192
Db 573 GGTGAAGTTTCAAGTGATGATGACCCAGTACATCAAG 608

RESULT 2

US-09-828-310-1/c
; Sequence 1, Application US/09828310
; Patent No. 6689939
; GENERAL INFORMATION:
; APPLICANT: COSTA E SILVA, OSWALDO DA
; APPLICANT: BOHNER, HANS J.
; APPLICANT: VAN THIELEN, NOCHA
; APPLICANT: CHEN, ROUYING
; TITLE OF INVENTION: GTP BINDING STRESS-RELATED PROTEINS AND METHODS OF USE
; FILE REFERENCE: 16313-0039
; CURRENT APPLICATION NUMBER: US/09/828,310
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/196,001
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 805
; TYPE: DNA
; ORGANISM: Physcomitrella patens
US-09-828-310-1

Alignment Scores:

Pred. No.: 7.57e-120 Length: 805
Score: 998.00 Matches: 192
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-688-481-11 (1-192) x US-09-828-310-1 (1-805)

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Db 753 ATGTTCTTGTAGATTGGTTTACGGCTTCTTCGCGAGCATAGGGCTGTGGCAAGAGAG 694
Qy 21 AlAlaValIleLeuPheLeuGlyLeuAspAsnAlaGlyLeuThrThrLeuLeuHisMetLeu 40
Db 693 GCCAAATCCGTGTTCTGGGTCTCGACATGCTGGCAAGACTACTCTTCTGCAATGCTC 634
Qy 41 LysAspGlyLysLeuGlyGlnHisGlnProThrGlnTygProThrSerGlnLysLeuSer 60
Db 633 AAGGATGAGAACTGGGGCAACATCAACCAACGAGTATCCAGCTGACAGAGATTGAGT 574
Qy 61 IleAsnArgValLysPheLysAlaPheAspLeuGlyGlyHisThrIleAlaArgVal 80
Db 573 ATCAACAGATGAGATTCAAGCATTCGATCGGTGGCCACACAACTCGTCGACGGGTG 514
Qy 81 TrpArgAspTygTygAlaLysValAspAlaIleValTygLeuValAspAlaValAspArg 100
Db 513 TGGAGGACTACTATGCTTAAGTGATGCTATGATGATCTGCGACGAGTGAACAGG 454
Qy 101 GluArgPheAlaGlySerLysGlyLeuAspSerLeuLeuSerAspAspSerLeuSer 120
Db 453 GAGGATTTCTGATGATCAAGAAAGAGCTCGATTCCTTCTCTCGAGCATTCCTGTCC 394
Qy 121 GlnValProValIleuValIleuGlyAsnLysIleAspIleProTygAlaSerSerGluAsp 140
Db 393 CAAGTTCTGTGCTGCTGCTGGGAAACAAAGATTGATCCGTAAGCTTCTTGAAGAC 334
Qy 141 GluLeuArgPheThrLeuGlyLeuThrMetThrThrGlyGlyThrValAsnLeuGly 160
Db 333 GAGTTCGGTTCACACTGGGTGACCATGACCATGCTGTAAAGAAACGTTAACTGGGA 274
Qy 161 AspSerAsnIleArgProIleGlnValPheMetCysSerIleValArgLysMetGlyTyr 180
Db 273 GATACCAACATTCGCGCCATTTGAGGTTTCATGTGCAATATTGTGCGCAATGGGGTAC 214
Qy 181 GlyGlnGlyPheLysTrpMetThrGlnTygIleLys 192
Db 213 GGTGAAGTTTCAAGTGATGATGACCCAGTACATCAAG 178

RESULT 3

US-09-270-767-13105
; Sequence 13105, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 13105
; LENGTH: 3191
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-13105

Alignment Scores:

Pred. No.: 5.5e-77 Length: 3191
Score: 674.50 Matches: 127
Percent Similarity: 79.69% Conservative: 26
Best Local Similarity: 66.15% Mismatches: 38
Query Match: 67.59% Indels: 1
DB: 3 Gaps: 1

US-10-688-481-11 (1-192) x US-09-270-767-13105 (1-3191)

Qy 1 MetPheLeuValAspTrpPheTyrglyPheLeuAlaSerIleGlyLeuTrpGlnLysGln 20
Db 174 ATGTTCACTGGACTGGTTCACCGAGTGTGGATATCCTGGGTCTGTGAAAAAGTCT 233

QY	21	AlaIleuIleuHeuHeuIeuIeuAbaPaNaIaGlyVtStrThrIleuLeuHiMeIeu	40
Db	234	GGCAAAATATATTGTTCTCGGCGCTGGATATAGCTGGCAAAACACACTTTGCATATGCTC	293
QY	41	LYeAspGIuLysIeuGIyGIhniGIInProThrGIInTyProThSerGIuLysSer	60
Db	294	AAAGATGATATAGCTGGCGGCGAGCATGTGGCCACACATGCATCCAACTCCGAGAGCTGTCC	353
QY	61	ILeAsnArgValIysPheIysAlaPheAspIeuGIyGIhIsthIleAlaArgVal	80
Db	354	ATCGCAACAATGGCGCTTCACTACATTCGACTTGGGTGGCAACACTCAAGGCACGACGCTC	413
QY	81	TrpArgAspTyTrpValAlaIysValAspAlaIleValTyTrLeuValAspAlaValAspArg	100
Db	414	TGGAAAGACTACTCTCCCTGCTGGACGGCACTGTTCTTATATGACGCTTGGAGACCGT	473
QY	101	GIuArgPheAlaGluSerLysLysGIuLeuAspSerLeuLysSerAspAspSerLeuSer	120
Db	474	GCGCGCTTCCAGAGAGACAAACGAGCTGGATTGCTGCTCACGAGAGAGCGCGCTGTCC	533
QY	121	GIuValProValIeuValIeuGIyAsnLysIleAspIleProTyTrAlaSerSerGIuAsp	140
Db	534	AACGCGCCCGTCTCATATTGGGCACAACAATCGATTAAGCCCGCGCGCGCTACGAGAGAT	593
QY	141	GIuLeuArgPheThrIeuGIyLeu--ThrMetThrThrGIyLysGIyThrValAsnLeu	159
Db	594	GAGCTGAGAAACGTGTTCGGACTGTATCGATCAACACCGGCAAGGCAAGTTGCACGC	653
QY	160	GIYAspSerAsnIleArgProIleGIuValPheMetCysSerIleValArgLysMetGIy	179
Db	654	GCGATTTGGCCGCGCGCTCTCTGGAAATGTTCATGTGCTCGTGCTGAACGACGACGCGC	713
QY	180	TyrGIyGIuGIyPheLysTrpMetThrGIyTrIle	191
Db	714	TACGGCAGGGATTTCGTTGGCTGGCGCAAGTATATC	749

RESULT 4
US-09-533-559-6998
; Sequence 6998, Application US/09533559

```

1  APPLICANT: Randy M. Berka
2  APPLICANT: Michael M. Rey
3  APPLICANT: Jeffrey R. Shuster
4  APPLICANT: Sakari Kauppinen
5  APPLICANT: Ib Groth Clausen
6  APPLICANT: Peter Barke Olsen
7  TITLE OF INVENTION: Methods For Monitoring Multiple Genes
8  TITLE OF INVENTION: Expression
9  FILE REFERENCE: 5849.200-05
10 CURRENT APPLICATION NUMBER: US/09/533.559
11 CURRENT FILING DATE: 2000-03-22
12 EARLIER APPLICATION NUMBER: 09/273.623
13 EARLIER FILING DATE: 1999-03-22
14 NUMBER OF SEQ ID NOS: 7860
15 SOFTWARE: Fastseq For Windows Version 4.0
16 SEQ ID NO 6998
17 LENGTH: 716
18 TYPE: DNA
19 ORGANISM: Aspergillus oryzae
20 US-09-533-559-6998

```

Alignment Scores:		
Pred. No.:	1.62e-71	Length: 716
Score:	307.00	Method: Waterbury
		110

```
Percent Similarity: 78.01% Conservative: 30
Beet Local Similarity: 62.30% Mismatches: 40
Query Match: 62.63% Indels: 2
DB: 3 Gaps: 1
```

US-10-688-481-11 (1-192) X US-09-533-559-6998 (1-716)

Qy 1 MetPheLeuValAspTyrPheTyrGlyPheLeuAspSerIleGlyLeuTyrGlu 20
Db 95 ATGTGATCATTAACGTGTTACAGATGTCCTGGGCTCCCTGGGCTGCTCAACAAGCAC 154

Qy 21 AlaLeuIleLeuPheLeuGlyLeuAspAsnAlaGlyLeuThrLeuLeuHISMetLeu 40
Db 155 GCCAACCTCCTCTCTCCCTGGGCTCGACAAATGCCGAAAGAGAACCCCTTGCAATGTG 214

Qy 41 LysAspGluLysLeuGlyGlnHisGlnProThrGlnTyrProThrSerGluGluLeuSer 60
Db 215 AAAAAAGACGGGGTGGCCGGTCTTCAGCCACCCGCTACATCCGAGCTGGAGAGCTCGT 274

Qy 61 IleAsnArgValLysPheLysAlaPheAspLeuGlyHisThrIleAlaArgVal 80
Db 275 ATGCGAAACACACCGCTTCACTACCTTTGAGTGGGTGACACAGACGCCACGCTCTC 334

Qy 81 TrpArgAspTyrTyrAlaLysValAspAlaIleValTyrLeuValAspAlaValAspArg 100
Db 335 TGGAAAGCATATTTCCCGAAGTGAGCGGTATCGTTTCTCGTTGACGCCAAGAGACAC 394

Qy 101 GluArgPheAlaGluSerIleLysGluLeuAspSerLeuLeuSerAspAspSerLeuSer 120
Db 395 GACCGTTTCCCGAAGTCMAAGGCCAGAGCTCGACCTCTCCGTCAGAGGAGACTCGCC 454

Qy 121 GlnValProValLeuValLeuGlyAsnLysIleAspIleProTyrAlaSerSerGluAsp 140
Db 455 AAGGTCCTCTCTCATTTCTCGGCAACAAGATCGACACCCCGACGCCGTACGAGAGAC 514

Qy 141 GluLeuArgPheThrLeuGlyLeuThrMetThrThrGlyLysGlyThrValAsnLeuGly 160
Db 515 GAACCTAGACACACAGGTGGACTTCAACAGACCAAGGAAAGGCGCAAGTGCACCT--- 571

Qy 161 AspSerAsnIleArgProIleGluValPheMetCysSerIleValAlaGlybMetGlyTyr 180
Db 572 ---GAGGCGATCCGACCGATCAAGGCTTTCATGTGCAGTGTGTGATGAGACAGGGTTAC 628

Qy 181 GlyGluGlyPheLysTyrMetThrGlnTyrIle 191
Db 629 GGGGAGGATATCAAGGTGGGTGTGCCAATAAGCTT 661

RESULT 5
US-08-825-780-2
; Sequence 2, Application US/08825780

Patent No. 5834238
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Puri
TITLE OF INVENTION: NOVEL HUMAN GTP BINDING
TITLE OF INVENTION: ROTENIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/825,780
FILING DATE: Filed Herewith

PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-024 US

EARLIER APPLICATION NUMBER: 60/043,674
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,669
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,312
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,313
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,672
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,315
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/056,886
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,877
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,889
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,893
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,630
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,878
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,662
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,872
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,882
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,887
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,903
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,888
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,879
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,880
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,894
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,911
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,636
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,874
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,910
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,864
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,631
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,845
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,892
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,761
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/047,595
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,599
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,588
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,585
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,586
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,590

EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,594
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,589
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,593
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,614
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,578
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,576
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/056,632
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,664
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,876
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,875
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,862
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,887
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02

Alignment Scores:

Pred. No.: 8,26e-70 Length: 1228
Score: 614.50 Matches: 115
Percent Similarity: 77.44% Conservative: 36
Best Local Similarity: 58.97% Mismatches: 39
Query Match: 61.57% Indels: 5
DB: 3 Gaps: 3

US-10-688-481-11 (1-192) x US-09-149-476-285 (1-1228)

Qy 2 PheLeuValAspTrpPheTyPheGlyPhe-----LeuAlaSerIleGlyLeuTrp 17
Db 95 TTGATATTTGATTGATTTGACGTTTTCAGCAGTGTGTCATGATTTTATAGGATTATAT 154
Qy 18 GlnLysGlnAlaLysIleLeuPheLeuGlyLeuAspAsnAlaGlyLysThrThrLeuLeu 37
Db 155 AAGAAAACTGGTAACCTGATTCTTGTGATTGATTAATGCAGAAAAACACATTGCTA 214
Qy 38 HisMetLeuLysAspGlnLysLeuGlnHisGlnProThrGlnTyPProThrSerGlu 57
Db 215 CACATGCTAAAGATATGACACACTTGGACACATGTCACACATTACATCCACTTCGAA 274
Qy 58 GluLeuSerIleAsnArgValLysPheLysAlaPheAspLeuGlyGlnIsthTrileAla 77
Db 275 GAACGTACCATTCCTGCGACATGACGTTTACAACTTTGATCTGGGTGACATGTTCAAGCT 334


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; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Alignment Scores:
Pred. No.:      8,83e-70      Length:      1285
Score:          614.50      Matches:      115
Percent Similarity: 77.44%      Conservative: 36
Best Local Similarity: 58.97%      Mismatches:  39
Query Match:      61.57%      Indels:      5
DB:               3          Gaps:      3

US-10-668-481-11 (1-192) x US-09-149-476-146 (1-1285)

QY      2  PheLeuValAspTrpPheTyr--GlyPhe-----LeuAlaSerIleGlyLeuTrp 17
Dd      122 TTCAATATTGATTTGGATTATTACAGTGTTCACAGTGTTCACAGTTTATAGCATATAT 181
QY      18  GlnIysGluAlaIysIleLeuPheLeuGlyLeuAspAspAlaGlyIysThrThrLeuLeu 37
Dd      182 AAGAAACTGTAACTGATATTTCTTGATTTGATTAATGACGAGAAACAAACATTGCTA 241
QY      38  HisMetLeuIysAspGluIysLeuGlyGlnHisGlnProThrGlnIrrProThrSerGlu 57
Dd      242 CACATGCTAAAGATGACAGACTTGACACACATGTCACCACTTACATCATCCACTTCGAA 301
QY      58  GlnLeuSerIleAsnArgValIysPheIysAlaPheAspLeuGlyGlnIsthrlIeAla 77
Dd      302 GAACGACCATTTGCTGCGATGACGTACGCTTACCACTTTGATCTGGGTGGACATGTTCAAGCT 361
QY      78  ArgArgValITTPArgAspTyrTyrAlaIysValaAlaIleValTyrIleuValaAlaPa 97
Dd      362 CGAAGAGGTGTGAAACAACTACCTTCCTGCTATCAATGCGATTGTATTTGTGTGATTTGT 421
QY      98  ValAspArgGluArgPheAlaGlnSerIysGluLeuAspSerLeuSerLeuSerAspAsp 117
Dd      422 GCAGACCCGAAAGCGCTGTAGATGATCAAAAGAAAGAACTTGATTCACCTAATGACAGATGA 481
QY      118 SerLeuSerGlnValProValLeuValLeuGlyAsnIysIleAspIleProTyrAlaSer 137
Dd      482 ACCATGCTGTAATGTCCTATACCTGATTTCTTGGAATTAAGATGACAGACTGAAGCCATC 541
QY      138 SerGluAspGluLeuArgPheThrIleuGlyLeu---ThrMetThrThrGlyIysGlyThr 156
Dd      542 AGTGAAAGAGAGCTTGCAGAGATGTTGGTTATATGTGTACAGACAAACAGAAAGCGGAGCT 601
QY      157 ValAsnLeuGlyAspSerAsnIleArgProIleGlnValPheMetCysSerIleValArg 176
Dd      602 ATATCTCGAAAGAACTGAATGCCGACCCCTTAGAAGTTTCATGTATGATGTGTCCTCAA 661
QY      177 LysMetGlyTyrGlyGluGlyPheIysTrpMetThrGlnTyrIle 191
Dd      662 AGACAGGTTACGGAGAAAGGCTTCGGCTGGATGGACAGCATCATTT 706

RESULT 8
US-09-248-796A-6222
; Sequence 6222, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keitch Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409

```

PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 6222
LENGTH: 564
TYPE: DNA
ORGANISM: Candida albicans
US-09-248-796A-6222

Alignment Scores:
Pred. No.: 1,53e-66 Length: 564
Score: 585.50 Matches: 114
Percent Similarity: 77.35% Conservative: 26
Best Local Similarity: 62.98% Mismatches: 40
Query Match: 58.67% Indels: 1
DB: 3 Gaps: 1

US-10-688-481-11 (1-192) x US-09-248-796A-6222 (1-564)

QY 11 LeuAlaSerIleGlyLeuTTPGlnLysIleLeuPheLeuGlyLeuAspAsn 30
DB 22 TTATCATCATTAAGGATTATGAATTAACATGCCAAATTATTTAGGGTTAGATAT 81
QY 31 AlaGlySerThrThrLeuLeuHisMetLeuLysAspGlyLysLeuGlnHisGlnPro 50
DB 82 GCTGGTAAACTACTCTTTACATATATGTAAGAATGATAGTGGCCACTTACCA 141
QY 51 ThrGlnTyrProThrSerGluLysLeuSerIleAsnArgValLysPheLysAlaPheAsp 70
DB 142 ACATTACATCCACCTTCAGAAAGATTGGCCATTGATCAGTATTAATTACTTAT 201
QY 71 LeuGlyGlyHisThrIleAlaArgArgValTTPArgAspTyrTyrAlaLysValAspAla 90
DB 202 TTAGTGGACATCAACAAGCTAGAAGATTATGAAAGATTATTTCCCTGAAGTCAATGCT 261
QY 91 IleValTyrLeuValAspAlaValAspArgGluArgPheAlaGlnSerLysLeuGluLeu 110
DB 262 ATTGCTTTTAAAGTGAATGCTGATGATCCAAAGATTGCTGATCCAAAGCTGAATG 321
QY 111 AspSerLeuLeuSerAspAspSerLeuSerGlnValProValLeuValLeuGlyAsnLys 130
DB 322 GAAAGTTTATTAAAGATTGAAGATTGATGCAAGTTCCATTGTTATTTGGGTATATAG 381
QY 131 IleAspIleProTyrAlaSerSerGluAspGluLeuArgPheThrLeuGlyLeuThrMet 150
DB 382 ATTGATGTTCTACTGCGAGGGAATGGAATTGAATAATGCCCTTGATATATATAT 441
QY 151 ThrThrGlyLysGlyThrValAsnLeuGlyAspSerAsnIleArgProIleGluValPhe 170
DB 442 ACTACTGATAAGATGCTGTAATTCCTGAAGGACT--AGACCAATTGAAGGTGTT 498
QY 171 MetCysSerIleValArgLysMetGlyTyrGlyGlnGlyPheLysTTPMetThrGlnTyr 190
DB 499 ATGGTTCCGTTGTTATGATCTGATATGATATGATGATGATGATGATGATGATGATGAT 558
QY 191 Ile 191
DB 559 ATT 561

RESULT 9

US-09-016-434-913
Sequence 913, Application US/09016434
Patent No. 6500938

GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Sellhammer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESS: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA

COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREMITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 913:
SEQUENCE CHARACTERISTICS:
LENGTH: 903 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: TONSNOT01
CLONE: 735249
US-09-016-434-913

Alignment Scores:
Pred. No.: 5,35e-63 Length: 903
Score: 560.50 Matches: 111
Percent Similarity: 75.13% Conservative: 37
Best Local Similarity: 56.35% Mismatches: 42
Query Match: 56.16% Indels: 7
DB: 3 Gaps: 3

US-10-688-481-11 (1-192) x US-09-016-434-913 (1-903)

QY 2 PheLeuValAspTTPPheTyr---GlyPhe-----LeuAlaSerIleGlyLeuTTP 17
DB 215 TTATCTTGAAGGATGATCAATGCTTCAAGCTGCTCCAGTCTTGAAGCTGATAC 274
QY 18 GlnLysGlnAlaLysIleLeuPheLeuGlyLeuAspAsnIleGlyLysThrThrLeuLeu 37
DB 275 AAGAAATCTGAAAACCTTGATCTTGAAGTTGATATGCAAGCAAAACCACTCTTCT 334
QY 38 HisMetLeuLysAspGlyLysLeuGlyGlnHisGlnProThrGlnTyrProThrSerGlu 57
DB 335 CACATGCTCAAGATGACAGATTTGGCCACATGTTCCACATCACTACATCCAGATCA 394
QY 58 GluLeuSerIleAsnArgValLysPheLysAlaPheAspLeuGlyHisThrIleAla 77
DB 395 GAGCTACATTTGCTGGAATGACCTTTACAACTTTGATCTTGGGACAGACAGCA 454
QY 78 ArgArgValTTPArgAspTyrTyrAlaLysValAspAlaIleValIyrLeuValAspAla 97
DB 455 GCTGCTTTGGAATAATTTATCTCCAGCAATTATGATGATGATGATGATGATGATGAT 514
QY 98 ValAspArgGluArgPheAlaGlnSerLysLeuGlnLeuAspSerLeuLeuSerAspAsp 117
DB 515 GCAAGATCTTCTCCCTCGGAGATCCAAAGTTAAGCTTATATGATGATGATGATGAT 574
QY 118 SerLeuSerGlnValProValLeuValLeuGlyAsnLysIleAspIleProTyrAlaSer 137
DB 575 ACATATCCATATGCCAATCTTATCTTGGGTAACAAATGACAGAACAGATGATC 634
QY 138 SerGluAspGluLeuArgPheThrLeuGlyLeu---ThrMetThrThrGlyLysGlyThr 156

Db 635 AGTGAAGAAAACTCCGTGATATTGGCTTTATGACAGACCAAGGAAGGGAAT 694
Qy 157 ValAsnLeuGlyAspSerAniLeaArgProIleGluValPheMetCysSerIleValArg 176
Db 695 GTGACCCCTGAAGAGCTGAATGCTCGCCCATGAAAGTGTTCATGTGCAAGTGTCTCAAG 754
Qy 177 LyMetGlyTyArgIleGlu-GlyPheLeuSerPheMet-ThrGlnTyIle 191
Db 755 AGCGAAGGTTTACGGCGAGGGGTTTCCGCTCTTCCCAAGTATATT 801

RESULT 10
US-09-533-559-125
; Sequence 125, Application US/09533559
; Patent No. 6902887
; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rey
; APPLICANT: Jeffrey R. Shuster
; APPLICANT: Sakari Kauppinen
; APPLICANT: Ib Groth Clausen
; APPLICANT: Peter Bjarke Olsen
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE OF INVENTION: Expression
; FILE REFERENCE: 5849,200-US
; CURRENT APPLICATION NUMBER: US/09/533,559
; EARLIER FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 09/273,623
; NUMBER OF SEQ ID NOS: 7860
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 125
; LENGTH: 1700
; TYPE: DNA
; ORGANISM: Fusarium venenatum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1700)
; OTHER INFORMATION: n = A,T,C or G
US-09-533-559-125

Alignment Scores:
Pred. No.: 3,41e-60 Length: 1700
Score: 542.00 Matches: 112
Percent Similarity: 73.85% Conservative: 32
Best Local Similarity: 57.44% Mismatches: 46
Query Match: 54.31% Indels: 6
Gaps: 2

US-10-688-481-11 (1-192) x US-09-533-559-125 (1-1700)

Qy 1 MetPheLeuValAspTrpPheTyArgIlePheLeuAlaSerIleGlyLeuTrpGlnTyGlu 20
Db 112 ATGTGATGATCTCAACGTGCTCTACGATGCTGTCTGCTCCCTGGGCTGCTCAACAAGCAC 171
Qy 21 AlaIleValIleLeuPheLeuGlyLeuAspAsnAlaGlyIleThrThrLeuLeuHisMetLeu 40
Db 172 GCAAGGCTGCTTCTTCCTGCGTCTTGACACGCGGAAAGACTACTCTTCTCCACATGCTG 231
Qy 41 LyAspGluTyLeuGlyGlnHisGlnProThrGlnTyProThrSerGluGluLeuSer 60
Db 232 AAGAAGACCGCTGTGTCATTTCCAGCCCACTTTCAACCCCACTCCAGAGAGCTTGTCT 291
Qy 61 IleAsnArgValIlePheLeuValAlaPheAspLeuGlyGlnHisThrIleAlaArgArgVal 80
Db 292 ATTTGTAAGCTCGCTTCCACCACTTTCGATCTTGTCGTCATCAACAGCGCCGACGATC 351
Qy 81 TrpArgAspTyArgIleValAlaValAspAlaIleValIleValLeuValAspAlaValAspArg 100
Db 352 TGGGGCATTAATCTTCCCGGAGTCAACGCTGCTCTTCTTCAACGCGCAAGAGACAC 411
Qy 101 GluArgPheAlaGluSerIleValGlyLeuAspSerLeuLeuSerLeuSer 120
Db 412 GAGGATTTGGTGTGANGCTAAGGCGAGCTGACGCGCTCTCTCTATGAGAAGAACTTCC 471

Qy 121 GlnValProValLeuValLeuGlyAsnTyIleAspIleProTyAlaSerSerGluAsp 140
Db 472 AAGTTCCTCTTGTCTATCTTCCGCAACAGATGACCA-CCGATATCCCTCTCCGAAGAC 530
Qy 141 GluLeuArgPheThrLeuGlyLeuThrMetThrThrGlyIleGlyIleValLeuLeuGly 160
Db 531 GAAATCGACACCAACTCGGGCTTACCAACAACCGGTAAAGGCAAGGCTCAACTT--- 587
Qy 161 AspSerAniLeaArgProIleGluValPheMetCysSerIleValAlaArgIleMet-GlyTy 180
Db 588 ---GAGGCGATCGACCTTATGAGCTTTCATGTGCTCANTATTTGCGCCAAAGTTA 644
Qy 180 rGlyGluGlyPheLeuS-----TrpMetThrGlnTyIleLeu 192
Db 645 CGGGAGANGGTATTAACCTGTGTTGTCACAGNTATGCTTAAG 687

RESULT 11
US-09-621-976-458
; Sequence 458, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Joberet, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent .pm
; SEQ ID NO 458
; LENGTH: 378
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 119..376
; NAME/KEY: misc_feature
; LOCATION: 143,318,332
; OTHER INFORMATION: n=a, g, c or t
US-09-621-976-458

Alignment Scores:
Pred. No.: 6,58e-41 Length: 378
Score: 386.00 Matches: 72
Percent Similarity: 89.53% Conservative: 5
Best Local Similarity: 83.72% Mismatches: 9
Query Match: 38.68% Indels: 0
Gaps: 0

US-10-688-481-11 (1-192) x US-09-621-976-458 (1-378)

Qy 1 MetPheLeuValAspTrpPheTyArgIlePheLeuAlaSerIleGlyLeuTrpGlnTyGlu 20
Db 119 ATGTTCTGTGTGACCTGTTCTTATNGGCTGCTCATTCGTTGGCTGTGGCAAGAG 178
Qy 21 AlaIleValIleLeuPheLeuGlyLeuAspAsnAlaGlyIleThrThrLeuLeuHisMetLeu 40
Db 179 GCTAAGATCTCTTCTTCTGCGCTCGAACAAGCGGGAAGACCACTCTCCACATGCTG 238
Qy 41 LyAspGluTyLeuGlyGlnHisGlnProThrGlnTyProThrSerGluGluLeuSer 60
Db 239 AAGGACGAGCGGCTCTTACAGCACCGCAACCGCACTATCCCAAGTCAGAGAGTTGAGC 298
Qy 61 IleAsnArgValIlePheLeuValAlaPheAspLeuGlyGlnHisThrIleAlaArgArgVal 80
Db 299 ATCGGAGATCAAGTTCACAGGCTTTCGACTTNGGGGCCACCAAGATTCGCGCGCTC 358
Qy 81 TrpArgAspTyArgIleAla 86
Db 359 TGAAGAGACTACTTCGCC 376

RESULT 12
US-09-621-976-445
Sequence 445, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jodere, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 445
LENGTH: 504
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 141..503
US-09-621-976-445

Alignment Scores:
Pred. No.: 1,06e-36 Length: 504
Score: 355.00 Matches: 68
Percent Similarity: 74.79% Conservative: 21
Best Local Similarity: 57.14% Mismatches: 26
Query Match: 35.57% Indels: 4
Gaps: 2

US-10-688-481-11 (1-192) x US-09-621-976-445 (1-504)

Qy 2 PheLeuValAspTrpPheTyr---GlyPhe-----LeuAlaSerIleGlyLeuTrp 17
Db 147 TTCATCTTGAAGTGGATCTTACAAATGGCTTCAAGCACTGCTCCAGTCTCTAGAGCTGAC 206
Qy 18 GlnLysGluAlaLysIleLeuPheLeuGlyLeuAspAsnAlaGlyLysThrThrLeuLeu 37
Db 207 AAGAAATCGAAAAAAGCTGTATCTTAGCTTGGATATGACAGCAAAACACCTCTCTT 266
Qy 38 HisMetLeuLysAspGluLysLeuGlyGlnHisGlnProThrGlnTyrProThrSerGlu 57
Db 267 CACATGCTCCAAAGATGACAGATGGGCAACATGTTCCAAACATCAATCCACATCAGAA 326
Qy 58 GluLeuSerIleAsnArgValLysPheLysAlaPheAspLeuGlyGlyHisThrIleAla 77
Db 327 GAGCTAAACATTCGCGAATGACCTTTCAACTTTGATCTTGGTGGCAGCAGACACR 386
Qy 78 ArgArgValTTPArgAspTyrTyrAlaLysValAspAlaIleValTyrLeuValAspAla 97
Db 387 CGTGGCGTTTGGAAAAATTAATCTCCACAGCAATTAATGGATGTTCTTCTGTGGACTGT 446
Qy 98 ValAspArgGluArgPheAlaGluSerLysGlyLeuAspSerLeuLeuSerAsp 116
Db 447 GCAGATCATCTTCGCTCGTGGAAATCCAAAGTTGAGCTTAATGATGACTGAT 503

RESULT 13

US-09-313-294A-3554
Sequence 3554, Application US/09313294A
Patent No. 6476212
GENERAL INFORMATION:
APPLICANT: Laligudi, Raghunath V.
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
FILE REFERENCE: PU-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
NUMBER OF SEQ ID NOS: 1999-05-14
SOFTWARE: PERL Program
SEQ ID NO 3554
LENGTH: 271

TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6476212 700611878H1
NAME/KEY: unautre
LOCATION: 220, 249, 262, 270
OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-3554

Alignment Scores:
Pred. No.: 9.72e-31 Length: 271
Score: 306.00 Matches: 67
Percent Similarity: 84.62% Conservative: 10
Best Local Similarity: 73.63% Mismatches: 12
Query Match: 30.66% Indels: 4
Gaps: 1

US-10-688-481-11 (1-192) x US-09-313-294A-3554 (1-271)

Qy 102 ArgPheAlaGluSerLysGlyLeuAspSerLeuLeuSerAspAspSerLeuSerGln 121
Db 1 CGATTGCTGAATCAAAAAGAGCTGAGCGCTCTCTGTCAGATGATTCCTTGGCAAT 60
Qy 122 ValProValLeuValLeuGlyAsnLysIleAspIleProTyrAlaSerSerGluAspGlu 141
Db 61 GTTCATATTCCTCATCTTGGCAACAGATTGATATCCGTATGCTGCTCTGAGAGAGAG 120
Qy 142 LeuArgPheThrLeuGlyLeuThr---MetThrGlyLysGlyThrValAsn-LeuGlu 160
Db 121 CTGGCGATACCTCAGGCTTTAGCACTTCAACACCGGAAAGGCAAGTCAACCTTGGG 180
Qy 160 YAspSerAsnIleArgProIleGluValPheMetCysSerIleValArgLysMetGlyTy 180
Db 181 CGATTCGAATGTCGCGACACTGAGGT-TTCATGTGAT-GTGTTCGCAAGATGGGGCT 238
Qy 180 rGlyGluGlyPheLysTrpMetThrGlnTyr 190
Db 239 AGCGATGATNTCAAGTGGGGCTTCCCAATAC 269

RESULT 14

US-09-016-434-501
Sequence 501, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Sellhammer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESS: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071

REFERENCE/DOCKET NUMBER: PA-0002 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 855-0555
 TELEFAX: (650) 845-4166
 INFORMATION FOR SEQ ID NO: 501:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 262 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: PROSNON01
 CLONE: 2278736
 US-09-016-434-501

Alignment Scores:
 Pred. No.: 1.2e-27 Length: 262
 Score: 282.00 Matches: 52
 Percent Similarity: 79.76% Conservative: 15
 Best Local Similarity: 61.90% Mismatches: 17
 Query Match: 28.26% Indels: 0
 DB: 3 Gaps: 0

US-10-688-481-11 (1-192) x US-09-016-434-501 (1-262)

QY 11 LeuAlaSerIleGlyLeuTrpGlnLysGluAlaLysIleLeuPheLeuGlyLeuAspAsn 30
 DB 11 CTACAGCTTTTATATATATATAGAAAACTGTAACTGGATTTCTTGATTTGGATTAAT 70
 QY 31 AlAGLYeThrThrLeuLeuHisMetLeuLysAspGluLysLeuGlyGlnHisGlnPro 50
 DB 71 GCAGGAAAAACAACATTGCTACACATGCTAAAGATACAGACTTGGACAACATGCCA 130
 QY 51 ThGInTrProThrsSerGlnLysSerIleHisnArgValLysPheLysAlaPheAsp 70
 DB 131 ACATTACATCCCACTCCGAAGAACTGACCATTTGCTGACGTTTACAACTTTTGAT 190
 QY 71 LeuGlyGlyHisThrIleAlaArgArgValTrpArgAspTrpTrpAlaLysValAspAla 90
 DB 191 CTGGGTGACATGTTCAAGCTCGAAGAGTGTGGAAAACTACCTTCTGCTATCAATGCC 250
 QY 91 IleValTrpLeu 94
 DB 251 ATTGTATTCTG 262

RESULT 15
 US-09-949-016-3194
 ; Sequence 3194, Application US/09949016
 ; Patent No. 681239
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; FILE REFERENCE: CLO01307
 ; CURRENT APPLICATION NUMBER: US/09/949, 016
 ; PRIORITY FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIORITY FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIORITY FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3194
 ; LENGTH: 968
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-949-016-3194

Alignment Scores:
 Pred. No.: 5.73e-26 Length: 968
 Score: 275.50 Matches: 64

Percent Similarity: 53.93% Conservative: 39
 Best Local Similarity: 33.51% Mismatches: 77
 Query Match: 27.61% Indels: 11
 DB: 3 Gaps: 2

US-10-688-481-11 (1-192) x US-09-949-016-3194 (1-968)

QY 2 PheLeuValAspTrpPheTrpGlyPheLeuAlaSerIleGlyLeuTrpGlnLysGluAla 21
 DB 100 TTCATATATGGTGGCTTTTCTTCAAGTATATTTTCCAGTCTGTTGGAACTCGGAAATG 159
 QY 22 LysIleLeuPheLeuGlyLeuAspAsnAlaGlyLysThrThrLeuLeuHisMetLeuLys 41
 DB 160 AGAATTTTAATTTGGATTTAGTATGAGCAGGAAAAACCAATTTTGTATACATTACAA 219
 QY 42 AspGluLysLeuGlyGlnHisGlnProThrGlnTrpProThrsSerGlnLysSerIle 61
 DB 220 GTGGGAAAGTTGTTACTACTATACCTTACATTGATTAATGTAGACGGGTGACTAC 279
 QY 62 AsnArgValLysPheLysAlaPheAspLeuGlyGlyHisThrIleAlaArgArgValTrp 81
 DB 280 AAAAACCTTAATTTCCAACTGCGATTTAGAGGACAGACAGATTCAGGCCATCTGG 339
 QY 82 ArgAspTrpTrpAlaLysValAspAlaIleValTrpLeuValAspAlaValAspArgGlu 101
 DB 340 AGATGTACTATTCAACAACAGATGACGATTTATGTATGTAGACAGTTGTGACCGAGAC 399
 QY 102 ArgPheAlaGlnSerLysLysGluLeuAspSerLeuLeuSerAspAspSerLeuSerGln 121
 DB 400 CGAATTGGCATTTCCAAATCAGAGTTAGTTGTCATGTTGGAGAGAAAGAGCTGAGAAAA 459
 QY 122 ValProValLeuValLeuGlyAsnLysIleAspIleProTrpAlaSerSerGluAspGlu 141
 DB 460 GCCATTTTAGTGTGTTTGCATTAACAGACATGAAACAGCCATGACTTCTCAGAG 519
 QY 142 LeuArgPheThrLeuGlyLeuThrMetThrGlyLysGlyThrValAsnLeuGlyAsp 161
 DB 520 ATGGCAAAATTCACCTTGGTTACCTGCC-----TTGAAGGAC 555
 QY 162 SerAsnIleArgProIleGluValPheMetCysSerIleValArgLysMetGlyTrpGly 181
 DB 556 -----CGAAATGCGAGATATTCAAACGTCGCAACCAAGCAACCGGCTTGAT 606
 QY 182 GluGlyPheLysTrpMetThrGlnTrpLys 192
 DB 607 GAGCAATGGAATGCAATTGAAACATTAAAAA 639

Search completed: December 9, 2005, 03:52:43
 Job time : 173 secs

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OM protein - nucleic search, using frame_plus.p2n model

Run on: December 9, 2005, 01:42:26 ; Search time 792 Seconds
(without alignments)
2004.698 Million cell updates/sec

Title: US-10-688-481-11
Perfect score: 998
Sequence: 1 MFVLVDFVFGFLASIGLWQKE.....SIVRKMYGSGFGKMTQYIK 192

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues
Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=Published Applications NA Main -OPMT=faeta -STUFF=p2n.rnpbm
-MIMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1
-MATRIX=blomsun62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct
-THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptco -NORM=ext
-HEPFSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOR=6 -DELEXT=7

Database : Published Applications_NA_Main:*
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7: /cg2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
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9: /cg2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cg2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	998	100.0	667	3	US-09-828-310-6
2	998	100.0	667	8	US-10-688-481-6
3	998	100.0	805	3	US-09-828-310-1
4	998	100.0	805	8	US-10-688-481-1
5	880.5	88.2	955	7	US-10-425-114-21639
6	880.5	88.2	966	7	US-10-425-114-13536
7	880.5	88.2	1017	7	US-10-425-114-33360

8	880.5	88.2	1070	8	US-10-425-115-98353	Sequence 98353, A
9	880.5	88.2	1334	8	US-10-425-115-98354	Sequence 98354, A
10	877.5	87.9	954	7	US-10-767-701-13805	Sequence 13805, A
11	872.5	87.4	1184	7	US-10-437-963-45082	Sequence 45082, A
12	867.5	86.9	1164	7	US-10-425-114-26805	Sequence 26805, A
13	864.5	86.6	1047	8	US-10-767-795-1304	Sequence 1304, A
14	862.5	86.4	928	7	US-10-767-701-15389	Sequence 15389, A
15	862.5	86.4	986	7	US-10-425-114-15389	Sequence 20343, A
16	862.5	86.4	991	7	US-10-424-599-13515	Sequence 13515, A
17	862.5	86.4	998	7	US-10-425-114-7242	Sequence 7242, A
18	862.5	86.4	1051	7	US-10-425-114-20291	Sequence 20291, A
19	862.5	86.4	1073	7	US-10-425-114-378	Sequence 378, A
20	862.5	86.4	1117	7	US-10-425-114-27102	Sequence 27102, A
21	862.5	86.4	1221	8	US-10-425-115-143342	Sequence 143342, A
22	862.5	86.4	1337	8	US-10-425-115-143340	Sequence 143340, A
23	862.5	86.4	1645	8	US-10-425-115-143343	Sequence 143343, A
24	859.5	86.1	1198	7	US-10-425-114-11886	Sequence 11886, A
25	859.5	86.1	1332	7	US-10-424-599-13513	Sequence 13513, A
26	856.5	85.8	1036	7	US-10-424-599-31596	Sequence 31596, A
27	856.5	85.8	1191	7	US-10-424-599-39806	Sequence 39806, A
28	853.5	85.5	807	8	US-10-767-795-1302	Sequence 1302, A
29	852.5	85.4	1688	7	US-10-437-963-58339	Sequence 58339, A
30	843.5	84.5	1164	7	US-10-424-599-32367	Sequence 32367, A
31	842.5	84.4	994	8	US-10-767-795-1303	Sequence 1303, A
32	836.5	83.8	764	7	US-10-424-599-32368	Sequence 32368, A
33	833.5	83.7	1303	8	US-10-425-115-143338	Sequence 143338, A
34	823.5	82.5	675	3	US-09-770-149-379	Sequence 379, A
35	820.5	82.2	954	7	US-10-437-963-45083	Sequence 45083, A
36	815.5	81.7	532	7	US-10-021-323-15172	Sequence 15172, A
37	768.5	77.0	1066	7	US-10-424-599-142530	Sequence 142530, A
38	758	74.6	660	7	US-10-437-963-20654	Sequence 20654, A
39	744.5	74.6	811	8	US-10-425-115-140955	Sequence 140955, A
40	725.5	72.7	569	7	US-10-021-323-3674	Sequence 3674, A
41	698.5	70.0	603	7	US-10-021-323-11457	Sequence 11457, A
42	674.5	67.6	992	10	US-11-097-144-15608	Sequence 15608, A
43	665.5	66.7	570	8	US-10-425-115-12354	Sequence 12354, A
44	627	62.8	570	5	US-10-128-714-2426	Sequence 2426, A
45	625	62.6	716	8	US-10-653-047-6998	Sequence 6998, A

ALIGNMENTS

RESULT 1
US-09-828-310-6
; Sequence 6, Application US/09828310
; Patent No. US2002006124A1
; GENERAL INFORMATION:
; APPLICANT: COSTA E SILVA, OSWALDO DA
; APPLICANT: BOHNET, HANS J.
; APPLICANT: VAN THIELEN, NOCHA
; APPLICANT: CHEN, ROUYING
; TITLE OF INVENTION: GTP BINDING STRESS-RELATED PROTEINS AND METHODS OF USE
; FILE REFERENCE: 16313-0039
; CURRENT APPLICATION NUMBER: US/09/828,310
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/196,001
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 667
; TYPE: DNA
; ORGANISM: Physcomitrella patens
; US-09-828-310-6

Alignment Scores:
Pred. No.: 1,08e-116
Score: 998.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 3
Length: 667
Matches: 192
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-10-688-481-11 (1-192) x US-09-828-310-6 (1-667)

Qy 1 MetPheLeuValAspTrpPheTyrGlyPheLeuAlaSerIleGlyLeuTrpGlnLysGlu 20
Db 33 ATGTTTCTTGTAATGGTTTACGGCTTCTTCCAGCATAGGGCTGTGGCAAGAGAG 92

Qy 21 AlaLysIleLeuPheLeuGlyLeuAspAsnAlaGlyLysThrThrLeuLeuHisMetLeu 40
Db 93 GCCAAATCTCGTTTCTGGGCTCGACAAATGCTGGCAAGACTACTCTTCTGCACATGCTC 152

Qy 41 LysAspGluLysLeuGlyGlnHisGlnProThrGlnTyrProThrSerGluGluLeuSer 60
Db 153 AAGGATGAGAACTGGGGCAACATCAACCAACGATCCAAAGTCAAGAGAGTTGAGT 212

Qy 61 IleAsnArgValLysPheLysAlaPheAspLeuGlyGlyHisThrIleAlaArgVal 80
Db 213 ATCAACAGAGTGAAGTTCAAGCATTCGATCTGGGTGGCCACAAATCGCTCCAGCGCTG 272

Qy 81 TrpArgAspTyrTyrAlaLysValAspAlaIleValTyrLeuValAspAlaValAspArg 100
Db 273 TGGAGGAGACTACTATGCTTAAGTGATGCTATGATCTCGTCCAGCGAGTACAGG 332

Qy 101 GluArgPheAlaGluSerLysLysGluLeuAspSerLeuLeuSerAspAspSerLeuSer 120
Db 333 GAGAGATTGCTGAGTCAAGAAAGAGCTCGATTCTCTCTCCGACGATTCTGTCTCC 392

Qy 121 GlnValProValLeuValLeuGlyAsnLysIleAspIleProTyrAlaSerSerGluAsp 140
Db 393 CAATTCCTGTGCTCGTCTCGGAAACAAAGATTGATCCCGTACCGCTTCTTGAAGAC 452

Qy 141 GluLeuArgPheThrLeuGlyLeuThrMetThrThrGlyLysGlyThrValAsnLeuGly 160
Db 453 GAGTTGGGTTCAACCTGGGTTGACCATGACCACTGGTAAAGAAACGGTGAACCTGGGA 512

Qy 161 AspSerAsnIleArgProIleGluValPheMetCysSerIleValArgLysMetGlyTyr 180
Db 513 GATAGCAACATTCGGCCCATTTGAGGTTTCATGTGCAGTATGTGGCAAAATGGGGTAC 572

Qy 181 GlyGluGlyPheLysTrpMetThrGlnTyrIleLys 192
Db 573 GGTGAAGGTTCAAGTGATGATCAACCACTACATCAAG 608

RESULT 2

US-10-688-481-6

Sequence 6, Application US/10688481

Publication No. US20040194163A1

GENERAL INFORMATION:

APPLICANT: COSTA E SILVA, OSWALDO DA

APPLICANT: BOHNERT, HANS J.

APPLICANT: VAN THIELEN, NOCHA

APPLICANT: CHEN, ROUYING

TITLE OF INVENTION: GTP BINDING STRESS-RELATED PROTEINS AND METHODS OF USE

TITLE OF INVENTION: IN PLANTS

FILE REFERENCE: 16313-0039

CURRENT APPLICATION NUMBER: US/10/688,481

CURRENT FILING DATE: 2003-10-17

PRIOR APPLICATION NUMBER: 60/196,001

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 50

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 6

LENGTH: 667

TYPE: DNA

ORGANISM: Physcomitrella patens

US-10-688-481-6

Alignment Scores:

Pred. No.: 1,08e-116 Length: 667

Score: 998.00 Matches: 192

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 8 Gaps: 0

US-10-688-481-11 (1-192) x US-10-688-481-6 (1-667)

Qy 1 MetPheLeuValAspTrpPheTyrGlyPheLeuAlaSerIleGlyLeuTrpGlnLysGlu 20
Db 33 ATGTTTCTTGTAATGGTTTACGGCTTCTTCCAGCATAGGGCTGTGGCAAGAGAG 92

Qy 21 AlaLysIleLeuPheLeuGlyLeuAspAsnAlaGlyLysThrThrLeuLeuHisMetLeu 40
Db 93 GCCAAATCTCGTTTCTGGGCTCGACAAATGCTGGCAAGACTACTCTTCTGCACATGCTC 152

Qy 41 LysAspGluLysLeuGlyGlnHisGlnProThrGlnTyrProThrSerGluGluLeuSer 60
Db 153 AAGGATGAGAACTGGGGCAACATCAACCAACGATCCAAAGTCAAGAGAGTTGAGT 212

Qy 61 IleAsnArgValLysPheLysAlaPheAspLeuGlyGlyHisThrIleAlaArgVal 80
Db 213 ATCAACAGAGTGAAGTTCAAGCATTCGATCTGGGTGGCCACAAATCGCTCCAGCGCTG 272

Qy 81 TrpArgAspTyrTyrAlaLysValAspAlaIleValTyrLeuValAspAlaValAspArg 100
Db 273 TGGAGGAGACTACTATGCTTAAGTGATGCTATGATCTCGTCCAGCGAGTACAGG 332

Qy 101 GluArgPheAlaGluSerLysLysGluLeuAspSerLeuLeuSerAspAspSerLeuSer 120
Db 333 GAGAGATTGCTGAGTCAAGAAAGAGCTCGATTCTCTCTCCGACGATTCTGTCTCC 392

Qy 121 GlnValProValLeuValLeuGlyAsnLysIleAspIleProTyrAlaSerSerGluAsp 140
Db 393 CAATTCCTGTGCTCGTCTCGGAAACAAAGATTGATCCCGTACCGCTTCTTGAAGAC 452

Qy 141 GluLeuArgPheThrLeuGlyLeuThrMetThrThrGlyLysGlyThrValAsnLeuGly 160
Db 453 GAGTTGGGTTCAACCTGGGTTGACCATGACCACTGGTAAAGAAACGGTGAACCTGGGA 512

Qy 161 AspSerAsnIleArgProIleGluValPheMetCysSerIleValArgLysMetGlyTyr 180
Db 513 GATAGCAACATTCGGCCCATTTGAGGTTTCATGTGCAGTATGTGGCAAAATGGGGTAC 572

Qy 181 GlyGluGlyPheLysTrpMetThrGlnTyrIleLys 192
Db 573 GGTGAAGGTTCAAGTGATGATCAACCACTACATCAAG 608

RESULT 3

US-09-828-310-1/c

Sequence 1, Application US/09828310

Patent No. US20020066124A1

GENERAL INFORMATION:

APPLICANT: COSTA E SILVA, OSWALDO DA

APPLICANT: BOHNERT, HANS J.

APPLICANT: VAN THIELEN, NOCHA

APPLICANT: CHEN, ROUYING

TITLE OF INVENTION: GTP BINDING STRESS-RELATED PROTEINS AND METHODS OF USE

TITLE OF INVENTION: IN PLANTS

FILE REFERENCE: 16313-0039

CURRENT APPLICATION NUMBER: US/09/828,310

CURRENT FILING DATE: 2001-04-06

PRIOR APPLICATION NUMBER: 60/196,001

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 50

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1

LENGTH: 805

TYPE: DNA

ORGANISM: Physcomitrella patens

US-09-828-310-1

Alignment Scores:

Pred. No.: 1,42e-116 Length: 805

Score: 998.00 Matches: 192

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0
US-10-688-481-11 (1-192) x US-09-828-310-1 (1-805)

```
QY 1 MetPheLeuValAspTrpPheTyrGlyPheLeuAlaSerIleGlyLeuTrpGlnLysGlu 20
DB 753 ATGTTTCTGTAGATTGGTTTACGGCTTTCTTGCGAGCATAGGGCTGTGGCAGAAGAG 694
QY 21 AlaLysIleLeuPheLeuGlyLeuAspAsnIleGlyLysThrThrLeuLeuHisMetLeu 40
DB 693 GCCAAATCTCTGTTCTGGCTTCGACAAATGCTGGCAAGACTACTCTTCTGCAATGCTC 634
QY 41 LysAspGluLysLeuGlyGlnHisGlnProThrGlnTyrProThrSerGlnLysLeuSer 60
DB 633 AAGGATGAGAACTGGGGCAACATCAACCAACGATATCCAGTCAGAGAGATTGAGT 574
QY 61 IleAsnArgValLysPheLysAlaPheAspLeuGlyGlyHisThrIleAlaArgArgVal 80
DB 573 ATCAACAGAGTGAAGTTCAAAAGCATTGCATCTGGGTGGCCACACATCGCTGACGCGTG 514
QY 81 TrpArgAspTyrTyrAlaLysValAspAlaIleValTyrLeuValAspAlaValAspArg 100
DB 513 TGGAGGACTACTATGCTAAAGTGAGTGTATAGTGTATCTCGTCCAGCAGTACAGCAG 454
QY 101 GluArgPheAlaGluSerLysGlyLeuAspSerLeuLeuSerAspAspSerLeuSer 120
DB 453 GAGAGATTGGCTGAGTCAAAGAAAGAGCTCGATTCTCTCTCCAGCATTCCTGTCTCC 394
QY 121 GlnValProValLeuValLeuGlyAsnLysIleAspIleProTyrAlaSerSerGluAsp 140
DB 393 CAAGTTCCTGTCTGCTCTCGTGGGAAACAGATTGATATCCGTAACGCTTCTTGAAGAC 334
QY 141 GluLeuArgPheThrLeuGlyLeuThrMetThrThrGlyLysGlyThrValAsnLeuGly 160
DB 333 GAGTTGCGGTTCACACTTGGGTGACCATGACCACTGTAAAGAAACGGTGAACCTGGGA 274
QY 161 AspSerAsnIleArgProIleGluValPheMetCysSerIleValArgLysMetGlyTyr 180
DB 273 GATAGCAACATTCGGCCCATGAGTTTTCATGTGCGATTTGTGGCAAAATGGGGTAC 214
QY 181 GlyGluGlyPheLysTrpMetThrGlnTyrIleLys 192
DB 213 GGTGAAGTTTCAAGTGAATGACCCAGTACATCAAG 178
```

RESULT 4

US-10-688-481-1/c
; Sequence 1, Application US/10688481
; Publication No. US20040194163A1
; GENERAL INFORMATION:
; APPLICANT: COSTA E SILVA, OSWALDO DA
; APPLICANT: BOHNER, HANS J.
; APPLICANT: VAN THIELEN, NOCHA
; APPLICANT: CHEN, ROUYING
; TITLE OF INVENTION: GTP BINDING STRESS-RELATED PROTEINS AND METHODS OF USE
; FILE REFERENCE: 16313-0039
; CURRENT APPLICATION NUMBER: US/10/688,481
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/196,001
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 805
; TYPE: DNA
; ORGANISM: Physcomitrella patens
; US-10-688-481-1

Alignment Scores:
Pred. No.: 1,42e-116 Length: 805
Score: 998.00 Matches: 192
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0
US-10-688-481-11 (1-192) x US-10-688-481-1 (1-805)

```
QY 1 MetPheLeuValAspTrpPheTyrGlyPheLeuAlaSerIleGlyLeuTrpGlnLysGlu 20
DB 753 ATGTTTCTGTAGATTGGTTTACGGCTTTCTTGCGAGCATAGGGCTGTGGCAGAAGAG 694
QY 21 AlaLysIleLeuPheLeuGlyLeuAspAsnIleGlyLysThrThrLeuLeuHisMetLeu 40
DB 693 GCCAAATCTCTGTTCTGGCTTCGACAAATGCTGGCAAGACTACTCTTCTGCAATGCTC 634
QY 41 LysAspGluLysLeuGlyGlnHisGlnProThrGlnTyrProThrSerGlnLysLeuSer 60
DB 633 AAGGATGAGAACTGGGGCAACATCAACCAACGATATCCAGTCAGAGAGATTGAGT 574
QY 61 IleAsnArgValLysPheLysAlaPheAspLeuGlyGlyHisThrIleAlaArgArgVal 80
DB 573 ATCAACAGAGTGAAGTTCAAAAGCATTGCATCTGGGTGGCCACACATCGCTGACGCGTG 514
QY 81 TrpArgAspTyrTyrAlaLysValAspAlaIleValTyrLeuValAspAlaValAspArg 100
DB 513 TGGAGGACTACTATGCTAAAGTGAGTGTATAGTGTATCTCGTCCAGCAGTACAGCAG 454
QY 101 GluArgPheAlaGluSerLysGlyLeuAspSerLeuLeuSerAspAspSerLeuSer 120
DB 453 GAGAGATTGGCTGAGTCAAAGAAAGAGCTCGATTCTCTCTCCAGCATTCCTGTCTCC 394
QY 121 GlnValProValLeuValLeuGlyAsnLysIleAspIleProTyrAlaSerSerGluAsp 140
DB 393 CAAGTTCCTGTCTGCTCTCGTGGGAAACAGATTGATATCCGTAACGCTTCTTGAAGAC 334
QY 141 GluLeuArgPheThrLeuGlyLeuThrMetThrThrGlyLysGlyThrValAsnLeuGly 160
DB 333 GAGTTGCGGTTCACACTTGGGTGACCATGACCACTGTAAAGAAACGGTGAACCTGGGA 274
QY 161 AspSerAsnIleArgProIleGluValPheMetCysSerIleValArgLysMetGlyTyr 180
DB 273 GATAGCAACATTCGGCCCATGAGTTTTCATGTGCGATTTGTGGCAAAATGGGGTAC 214
QY 181 GlyGluGlyPheLysTrpMetThrGlnTyrIleLys 192
DB 213 GGTGAAGTTTCAAGTGAATGACCCAGTACATCAAG 178
```

RESULT 5

US-10-425-114-21639
; Sequence 21639, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 21639
; LENGTH: 955
; TYPE: DNA
; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: LIB3354-056-D12_FLI
; US-10-425-114-21639

Alignment Scores:
Pred. No.: 1,65e-101 Length: 955

Score: 880.50 Matches: 163
Percent Similarity: 94.30% Conservative: 19
Best Local Similarity: 84.46% Mismatches: 10
Query Match: 88.23% Indels: 1
Gaps: 1

US-10-688-481-11 (1-192) x US-10-425-114-21639 (1-955)

```
QY 1 MetPheLeuValAspTrpPheTyrGlyPheLeuAlaSerIleGlyLeuTrpGlnLeuGlu 20
D 98 ATGTTCTGCTGGAGCTGCTGTCTATGAGGATGCTGCGATCGCTGGGCTGTGGCAAGAG 157
QY 21 AlaIysIleLeuPheLeuGlyLeuAspAsnAlaGlyIysThrThrLeuLeuHISMetLeu 40
D 158 GCTAAGATCCTCTTCTGGCTGCAACGCCGGCAAGACACCTCTCCATCATCTG 217
QY 41 LysAspGluLysLeuGlyGlnHISGlnProThrGlnTyrProThrSerGluGluLeuSer 60
D 218 AAGGACAGCGGCTCTGACAGCACAGCCAGCATGCCACCTCCAGAGAGTTGAGC 277
QY 61 IleAsnArgValLysPheLysAlaPheAspLeuGlyGlyIsthriIeAlaArgArgVal 80
D 278 ATCGCAGAGATCAAGTTCAAGCGCTTCGACCTTGGGGGCCACAGATCGCCCGCGTC 337
QY 81 TrpArgAspTyrTyrAlaLysValAspAlaIleValTyrLeuValAspAlaValAspArg 100
D 338 TGGAGGACTACTACCGCCAGAGTTGATGCTGTGTGATCTTGAGTGTGATGTTGACAG 397
QY 101 GluArgPheAlaGluSerLysLysGlyLeuAspSerLeuSerLeuSerAspAspSerLeuSer 120
D 398 GAACGTTTGGCCGATCGAAGAGAGAGCTCAATGCGCTTCTTGAGATGACTCCCTTGCA 457
QY 121 GluValProValLeuValLeuGlyAsnLysIleAspIleProTyrAlaSerSerGluAsp 140
D 458 AACGTTCTCTTCTCATCTACTGGCAACAGATTGACATCCCATACGCGCTTCAAGAGAG 517
QY 141 GluLeuArgPheThrLeuGlyLeuThr--MetThrThrGlyLysGlyThrValAsnLeu 159
D 518 GAGTGGAGTACTACTCTCGGCTGAGCACTTCAACCGGGAAGGGCAACGTGAACCTTG 577
QY 160 GlyAspSerAsnIleArgProIleGluValPheMetCysSerIleValArgLysMetGly 179
D 578 GCCGACTCCACGTCGCCGCCCTGAGATCTTCAATGTCAGATGTGTCGCAAGATGGC 637
QY 180 TyrGlyGluGlyPheLysTrpMetThrGlnTyrIleLys 192
D 638 TATGGCGAAGGCTTCAATGATGTCTCAGTACATCAAG 676
```

RESULT 6

US-10-425-114-13536
Sequence 13536, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 13536
LENGTH: 966
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LTB143-001-F4_FLI
US-10-425-114-13536

Alignment Scores:
Pred. No.: 1,686-101 Length: 966
Score: 880.50 Matches: 163
Percent Similarity: 94.30% Conservative: 19
Best Local Similarity: 84.46% Mismatches: 10
Query Match: 88.23% Indels: 1
Gaps: 1

US-10-688-481-11 (1-192) x US-10-425-114-13536 (1-966)

```
QY 1 MetPheLeuValAspTrpPheTyrGlyPheLeuAlaSerIleGlyLeuTrpGlnLeuGlu 20
D 130 ATGTTCTGCTGGAGCTGCTGTCTATGAGGATGCTGCGATCGCTGGGCTGTGGCAAGAG 169
QY 21 AlaIysIleLeuPheLeuGlyLeuAspAsnAlaGlyIysThrThrLeuLeuHISMetLeu 40
D 190 GCTAAGATCCTCTTCTGGCTGCAACGCCGGCAAGACACCTCTCCATCATCTG 249
QY 41 LysAspGluLysLeuGlyGlnHISGlnProThrGlnTyrProThrSerGluGluLeuSer 60
D 250 AAGGACAGCGGCTCTGACAGCACAGCCAGCATGCCACCTCCAGAGAGTTGAGC 309
QY 61 IleAsnArgValLysPheLysAlaPheAspLeuGlyGlyIsthriIeAlaArgArgVal 80
D 310 ATCGCAGAGATCAAGTTCAAGCGCTTTCGACCTTGGGGGCCACAGATCGCCCGCGTC 369
QY 81 TrpArgAspTyrTyrAlaLysValAspAlaIleValTyrLeuValAspAlaValAspArg 100
D 370 TGGAGGACTACTACCGCCAGAGTTGATGCTGTGTGATCTTGAGTGTGATGTTGACAG 429
QY 101 GluArgPheAlaGluSerLysLysGlyLeuAspSerLeuSerLeuSerAspAspSerLeuSer 120
D 430 GAACGTTTGGCCGATCGAAGAGAGAGCTTGAATGCTTTCAGATGACTCCCTTGCA 489
QY 121 GluValProValLeuValLeuGlyAsnLysIleAspIleProTyrAlaSerSerGluAsp 140
D 490 AACGTTCTCTTCTCATCTACTGGCAACAGATTGACATCCCATACGCGCTTCAAGAGAG 549
QY 141 GluLeuArgPheThrLeuGlyLeuThr--MetThrThrGlyLysGlyThrValAsnLeu 159
D 550 GAGTGGAGTACTACTCTCGGCTGAGCACTTCAACCGGGAAGGGCAACGTGAACCTTG 609
QY 160 GlyAspSerAsnIleArgProIleGluValPheMetCysSerIleValArgLysMetGly 179
D 610 GCCGACTCCACATCTCGGCCCTGAGATCTTCAATGTCAGATGTGTCGCAAGATGGC 669
QY 180 TyrGlyGluGlyPheLysTrpMetThrGlnTyrIleLys 192
D 670 TATGGCGAAGGCTTCAATGATGTCTCAGTACATCAAG 708
```

RESULT 7

US-10-425-114-33380
Sequence 33380, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 33380
LENGTH: 1017
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: UC-ZMFLMO17103B09_FLI

US-10-425-114-33380

Alignment Scores:

Pred. No.:	1, 8e-101	Length:	1017
Score:	880.50	Matches:	163
Percent Similarity:	94.30%	Conservative:	19
Best Local Similarity:	84.46%	Mismatches:	10
Query Match:	88.23%	Indels:	1
DB:	7	Gaps:	1

US-10-688-481-11 (1-192) x US-10-425-114-33380 (1-1017)

```
Qy      1 MetPheLeuValAspTrpPheTYRGLYPheLeuAlaSerIleGlyLeuTrpGlnYsglu 20
Db      111 ATGTTCTGCTGGAGCTGCTTCTATGGGCTGCTGGCACTGCTTGGGCTGCTGGAGAGAG 170
Qy      21 AlaLysIleLeuPheLeuGlyLeuAspAsnAlaGlyLysThrThrLeuLeuHISmetLeu 40
Db      171 GCTAAGATCCTCTTCTCTTGGCTCGACACGCGCGCAAGACACCTCTTCACATGCTG 230
Qy      41 LysAspGluLysLeuGlyGlnHisGlnProThrGlnTrpProThrSerGluGluLeuSer 60
Db      231 AAGGACGAGCGGCTCGTACAGCACACCGACGACGACGACGACGACGACGACGACGACGAC 290
Qy      61 IleAsnArgValLysPheLysAlaPheAspLeuGlyGlyHisThrIleAlaArgVal 80
Db      291 ATCGGACGATCAAGTTCAAGCGCTTGCACCTTGGGGCCACACAGATCCGCCCGCGCTC 350
Qy      81 TrpArgAspTrpTYRAlaLysValAspAlaIleValTYRLeuValAspAlaValAspArg 100
Db      351 TGGAGAGACTACTACCGCCAGGTTGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 410
Qy      101 GluArgPheAlaGlnSerIleLysGlyLeuAspSerLeuSerAspAspSerLeuSer 120
Db      411 GAACGTTTCCGAGTCGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 470
Qy      121 GlnValProValLeuValLeuGlyAsnLysIleAspIleProTYRAlaSerSerGluAsp 140
Db      471 AAGTTCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 530
Qy      141 GluLeuArgPheThrLeuGlyLeuThr--MetThrThrGlyLysGlyThrValAsnLeu 159
Db      531 GAGCTGAGTACTACTACCTCGGCTGAGCACTTCACACCGGAGAGGCAAGTGAACCTTG 590
Qy      160 GlyAspSerAsnIleArgProIleGluValPheMetCysSerIleValArgLysMetGly 179
Db      591 GCGGACTCCCATGTGCTCGGCTCGGAGATCTTCATGTGAGTGTGTGTGTGTGTGTGTGT 650
Qy      180 TYRGLYGLUGLYPHELYSTRPMETTRGINTYRILEYLS 192
Db      651 TATGGCGAAGGCTTCAAAATGATGTCTCAGTACATCAAG 689

RESULT 8
US-10-425-115-98353
; Sequence 98353, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425, 115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 98353
; LENGTH: 1070
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_21208C.1
```

US-10-425-115-98353

Alignment Scores:

Pred. No.:	1, 94e-101	Length:	1070
Score:	880.50	Matches:	163
Percent Similarity:	94.30%	Conservative:	19
Best Local Similarity:	84.46%	Mismatches:	10
Query Match:	88.23%	Indels:	1
DB:	8	Gaps:	1

US-10-688-481-11 (1-192) x US-10-425-115-98353 (1-1070)

```
Qy      1 MetPheLeuValAspTrpPheTYRGLYPheLeuAlaSerIleGlyLeuTrpGlnYsglu 20
Db      183 ATGTTCTGCTGGAGCTGCTTCTATGGGCTGCTGGCACTGCTTGGGCTGCTGGAGAGAG 242
Qy      21 AlaLysIleLeuPheLeuGlyLeuAspAsnAlaGlyLysThrThrLeuLeuHISmetLeu 40
Db      243 GCTAAGATCCTCTTCTCTTGGCTCGACACGCGCGCAAGACACCTCTTCACATGCTG 302
Qy      41 LysAspGluLysLeuGlyGlnHisGlnProThrGlnTrpProThrSerGluGluLeuSer 60
Db      303 AAGGACGAGCGGCTCGTACAGCACACCGACGACGACGACGACGACGACGACGACGACGAC 362
Qy      61 IleAsnArgValLysPheLysAlaPheAspLeuGlyGlyHisThrIleAlaArgVal 80
Db      363 ATCGGACGATCAAGTTCAAGCGCTTGCACCTTGGGGCCACACAGATCCGCCCGCGCTC 422
Qy      81 TrpArgAspTrpTYRAlaLysValAspAlaIleValTYRLeuValAspAlaValAspArg 100
Db      423 TGGAGAGACTACTACCGCCAGGTTGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 482
Qy      101 GluArgPheAlaGlnSerIleLysGlyLeuAspSerLeuSerAspAspSerLeuSer 120
Db      483 GAACGTTTCCGAGTCGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 542
Qy      121 GlnValProValLeuValLeuGlyAsnLysIleAspIleProTYRAlaSerSerGluAsp 140
Db      543 AAGTTCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 602
Qy      141 GluLeuArgPheThrLeuGlyLeuThr--MetThrThrGlyLysGlyThrValAsnLeu 159
Db      603 GAGCTGAGTACTACTACCTGCGCTGAGCACTTCACACCGGAGAGGCAAGTGAACCTTG 662
Qy      160 GlyAspSerAsnIleArgProIleGluValPheMetCysSerIleValArgLysMetGly 179
Db      663 GCGGATTCCAATGTGCTCGGCTCGGAGATCTTCATGTGAGTGTGTGTGTGTGTGTGTGT 722
Qy      180 TYRGLYGLUGLYPHELYSTRPMETTRGINTYRILEYLS 192
Db      723 TATGGCGAAGGCTTCAAAATGATGTCTCAGTACATCAAG 761

RESULT 9
US-10-425-115-98354
; Sequence 98354, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425, 115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 98354
; LENGTH: 1334
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_21209C.1
```

US-10-425-115-98354

Alignment Scores:
Pred. No.: 2,67e-101 Length: 1334
Score: 880.50 Matches: 163
Percent Similarity: 94.30% Conservative: 19
Best Local Similarity: 84.46% Mismatches: 10
Query Match: 88.23% Indels: 1
DB: 8 Gaps: 1

US-10-688-481-11 (1-192) x US-10-425-115-98354 (1-1334)

```
OY 1 MetPheLeuValAspTrpPheTyrGlyPheLeuAlaSerIleGlyLeuTrpGlnIlyGlu 20
Db ATGTTCTGCGAGCTGCTGTTCTATGGGGTGTCTGGCATCGCTTGGGCTGTGGCAGAGAG 330
OY 21 AlaValIleLeuPheLeuGlyLeuAspAsnAlaGlyLysThrThrLeuLeuHISMetLeu 40
Db GCTAAGATCTCTTCTTGGCTCGACACCGCCGAGACACCCTCTCTCCACATGCTG 390
OY 41 LysAspGluLysLeuGlyGlnHISGlnProThrGlnTyrProThrsSerGluGluLeuSer 60
Db AAGAGCAGCGCGCTCGTACAGACACGCGACGATGCCACGTCCAGAAAGATTGAGC 450
OY 61 IleAsnArgValLysPheLysAlaPheAspLeuGlyGlyHisThrIleAlaArgVal 80
Db ATCCGCGAGATCAAGTTCAGCGCTTCGATCGGGGCCACAGATCGCCCGCGCTC 510
OY 81 TrpArgAspTyrTyrAlaLysValAspAlaIleValTyrLeuValAspAlaValAspArg 100
Db TGGAAAGACTACAGCGCAGAGATTGATGCTGTGTGATCTGGAGATGCTGTGGACAG 570
OY 101 GluArgPheAlaGluSerLysLysGluLeuAspSerLeuLeuSerAspAspSerLeuSer 120
Db GAAGTTTTCGCGAGTCCGAGAGAGAGCTTATGCGCTCTTGCAGATGATCTCCCTTGA 630
OY 121 GlnValProValLeuValLeuGlyAsnLysIleAspIleProTyrAlaSerSerGluAsp 140
Db AACCTTCTCTTCCATCTACTGCGCAACAAAGATTGCATCCCATCGCGCTTCAGAGAG 690
OY 141 GluLeuArgPheThrIleuGlyLeuThr---MetThrThrGlyLysGlyTyrValAsnLeu 159
Db GAGTCAAGTACTACCTCGGCTGAGCACTTCAACACCGGAGGAGGCAACGTAACTTG 750
OY 160 GlyAspSerAsnIleArgProIleGlnValPheMetCysSerIleValArgLysMetGly 179
Db GCCGACTCCATGTCGGGCCCTCGAGATCTTCATGTCAGTGTGGTCCGCAAGATGGCC 810
OY 180 TyrGlyGluGlyPheLysTrpMetThrGlnTyrIleLys 192
Db TATGGCGAAGGCTTCAATGATGATGTCATGATCAATCAAG 849
```

RESULT 10

US-10-767-701-13805

Sequence 13805, Application US/10767701

Publication No. US20040172684A1

GENERAL INFORMATION:

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

FILE OF INVENTION: Plants and Uses Thereof For Plant Improvement

FILE REFERENCE: 38-21(53535)B

CURRENT APPLICATION NUMBER: US/10-767,701

CURRENT FILING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128

SEQ ID NO 13805

LENGTH: 954

TYPE: DNA

ORGANISM: Sorghum bicolor

FEATURE:

OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS2820_1

US-10-767-701-13805

Alignment Scores:
Pred. No.: 3,96e-101 Length: 954
Score: 877.50 Matches: 163
Percent Similarity: 94.30% Conservative: 19
Best Local Similarity: 84.46% Mismatches: 10
Query Match: 87.93% Indels: 1
DB: 7 Gaps: 1

US-10-688-481-11 (1-192) x US-10-767-701-13805 (1-954)

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OY 1 MetPheLeuValAspTrpPheTyrGlyPheLeuAlaSerIleGlyLeuTrpGlnIlyGlu 20
Db ATGTTCTGCGAGCTGCTGTTCTATGGGGTGTCTGGCATCGCTTGGGCTGTGGCAGAGAG 193
OY 21 AlaValIleLeuPheLeuGlyLeuAspAsnAlaGlyLysThrThrLeuLeuHISMetLeu 40
Db GCGAAGATCTCTTCTTGGCTCGACACCGCCGAGACACCCTCTCCACATGCTC 253
OY 41 LysAspGluLysLeuGlyGlnHISGlnProThrGlnTyrProThrsSerGluGluLeuSer 60
Db AAGAGCAGCGCGCTCGTACAGACACGCGACGATGCCACGTCCAGAAAGCTGAGC 313
OY 61 IleAsnArgValLysPheLysAlaPheAspLeuGlyGlyHisThrIleAlaArgVal 80
Db ATCCGCGAGATCAAGTTCAGCGCTTCGATCGGGGCCACAGATCGCCCGCGCTC 373
OY 81 TrpArgAspTyrTyrAlaLysValAspAlaIleValTyrLeuValAspAlaValAspArg 100
Db TGGAAAGACTACAGCGCAGAGATTGATGCTGTGTGATCTGGAGATGCTGTGGACAG 433
OY 101 GluArgPheAlaGluSerLysLysGluLeuAspSerLeuLeuSerAspAspSerLeuSer 120
Db GAGCGATTTCCAGAAATCAAAAAAGAGCTGATGCTCTCTGTGTGATTCCTTGGCC 493
OY 121 GlnValProValLeuValLeuGlyAsnLysIleAspIleProTyrAlaSerSerGluAsp 140
Db AATGTTCCATTTCTCATCTTGGCAACAAAGATTGATCCCATGCTGCTCGAAGAG 553
OY 141 GluLeuArgPheThrIleuGlyLeuThr---MetThrThrGlyLysGlyTyrValAsnLeu 159
Db GAGTCAAGTACTACCTCGGCTGAGCACTTCAACACCGGAGGAGGCAACGTAACTTG 613
OY 160 GlyAspSerAsnIleArgProIleGlnValPheMetCysSerIleValArgLysMetGly 179
Db GGTGACTCCATGTCGGGCCCTCGAGATCTTCATGTCAGTGTGGTCCGCAAGATGGCC 673
OY 180 TyrGlyGluGlyPheLysTrpMetThrGlnTyrIleLys 192
Db TACGATGATGTTCAAGTGGGTCTCCAGTACATCAAG 712
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RESULT 11

US-10-437-963-45082

Sequence 45082, Application US/10437963

Publication No. US2004012343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

APPLICANT: Wu, Wei

APPLICANT: Boukharov, Andrey A.

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53221)B

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 45082

LENGTH: 1184

TYPE: DNA

US-10-437-963-45082

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; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_48081.C.1
US-10-437-963-45082

Alignment Scores:
Pred. No.:      2,356-100      Length:      1184
Score:          872.50        Matches:      161
Percent Similarity: 93.78%    Conservative: 20
Best Local Similarity: 83.42% Mismatch:      11
Query Match:     87.42%      Indels:       1
DB:              7          Gaps:         1

US-10-688-481-11 (1-192) x US-10-437-963-45082 (1-1184)

QY      1 MetPheLeuValAspTrpPheTyrGlyPheLeuAlaSerIleGlyLeuTrpGlnIysGln 20
Db      148 ATGTTCTCGATTGACTGGCTTCTACGGGGGCTGGCTCGCTCGCTGGGCTGGGCAAGAG 207

QY      21 AAlaIleLeuPheLeuGlyLeuAspAsnAlaGlyIysThrThrLeuLeuHisIleLeu 40
Db      208 GCCAAGATCTCTTCTCGGCTTCACCAACGGCGGCACACCACTCTTCACATGTCTC 267

QY      41 LysAspGluIysLeuGlyGlnHisGlnProThrGlnTyrProThrSerGluGluSer 60
Db      268 AAGAGCGAGCGGCTCTGTGACGACACCGCCAGCGATGCCAGTCCAGTGGAGAGCTGACG 327

QY      61 IleAsnArgValIysPheIysAlaPheAspLeuGlyGlyHisThrIleAlaArgArgVal 80
Db      328 ATCGGCAGATCAATCAATCTTACAGCCCTTCGACCTCGGGGCGCACAGATGCCCGCGCGTC 387

QY      81 TrpArgAspTyrTyrAlaIysValAspAlaIleValTyrLeuValAspAlaValAspArg 100
Db      388 TGGAAAGCATCTACGCGCAAGGTCGATGCTGTGTATTGATGGATGCCCTGCAAG 447

QY      101 GluArgPheAlaGluSerIlyIysGluLeuAspSerLeuSerAspAspSerLeuSer 120
Db      448 GAACGGTTGGCGAGTTCGAGAGGAAGAACTCGATGCCCTCTTGCAAGCAATTCCTCAGCA 507

QY      121 GlnValProValLeuValLeuGlyIysAsnIysIleAspIleProTyrAlaSerSerGluAsp 140
Db      508 ACCGTCCTTCTCTGATATCTGCGAACAAGATCGACATCCATACGCCCGCTCGAGGAG 567

QY      141 GluLeuArgPheThrLeuGlyLeuThr--MetThrThrGlyIysGlyThrValAsnLeu 159
Db      568 GAACCTCCGCTACTACCTTGCTGTGAGCAACTCACACCGGTAAAGGCAACGTGAACCTA 627

QY      160 GlyAspSerAsnIleArgProIleGluValPheMetCysSerIleValArgIysMetGly 179
Db      628 GCCGACTCCACAGTCGCGGCTCTGAGAGATCTTCATGATGAGGTCGTCCGCAAGATGGAG 687

QY      180 TyrGlyGluGlyPheIysTrpMetThrGlnTyrIleIys 192
Db      688 TACGGCGAAGGCTTCMAATGATGTCCCGATCATCAAA 726

RESULT 12
US-10-425-114-26805
; Sequence 26805, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 26805

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; LENGTH: 1164
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4606-001-A8_FLI
US-10-425-114-26805

Alignment Scores:
Pred. No.: 9.91e-100 Length: 1164
Score: 867.50 Matches: 161
Percent Similarity: 93.26% Conservative: 19
Best Local Similarity: 83.42% Mismatches: 12
Query Match: 86.92% Indels: 1
DB: 7 Gaps: 1

US-10-688-481-11 (1-192) x US-10-425-114-26805 (1-1164)
QY 1 MetPheLeuValAspTrpPheTyrGlyPheLeuAlaSerIleGlyLeuTrpGlnIysGln 20
DB 259 ATGTTCTCGTGGAGCTGTTCTAAGGGGTGCTGGATGCTGGGCTGTGGAGAGAG 318
QY 21 AlaValIleuPheLeuGlyLeuAspAsnAlaGlyIysThrThrLeuLeuHisMetLeu 40
DB 319 GCTAAGATCTCTTCTCTTGCCCTCGACACAGCCGGCAGAACCACTCTCCATCATGCTG 378
QY 41 LysAspGlnIlybLeuGlyGlnHisGlnProThrGlnTyrProThrSerGlnIleuSer 60
DB 379 AAGGACGAGCGGCTCTGACACACACCGGACGAGTACCCACATCAGAAAGATTGAGC 438
QY 61 IleAsnArgValIysPheValAlaPheAspLeuGlyGlnHisThrIleAlaArgArgVal 80
DB 439 ATCGCGAGATCAAGTTAAAGGCGTTTGCACCTTGAGGGCCGACAGCCGCCGCGCTC 498
QY 81 TrpArgAspTyrTyrAlaIysValAspAlaIleValTyrLeuValAspAlaValAspArg 100
DB 499 TGGAAAGACTACTACGCCAAGGTTGATGCTGTGTGTACTTGATGGATGCTGTGCAAG 558
QY 101 GluArgPheAlaGluSerIleGlybGluLeuAspSerIleuSerIleuAspSerIleuSer 120
DB 559 GAACGTTTGGCCGAGTCAGAGAAAGAGCTTGATGTGGCTTTCAGAGATGATCTCCCTTGA 618
QY 121 GlnValProValIleuValLeuGlyIAsnIysIleAspIleProTyrAlaSerSerGluAsp 140
DB 619 AACGTTCTTCTTCATCTAGCGGCAACAAGATGATACATCCATACGCGGCTTCAGAGAG 678
QY 141 GluLeuArgPheThrLeuGlyLeuThr--MetThrThrGlyIlyGlyThrValAsnLeu 159
DB 679 GAGCTGAGGTACTACTCTGCGCTGAGCAACTCACACCGGGAAGGCAACGTGAACCTG 738
QY 160 GlyAspSerAsnIleArgProIleGluValPheMetCysSerIleValAlaArgIysMetGly 179
DB 739 GCCGACTCAACGTCGCCGCCCTCGAGATCTTCATGTACAGTGTGTGCGCAAGATGGGC 798
QY 180 TyrGlyGlnGlyPheIysTyrMetThrThrIleValIleVal 192
DB 799 TATGGCGAAGGCTTCAAAATGATGTCTCAGTACATCAAG 837

RESULT 13
US-10-767-795-1304
; Sequence 1304, Application US/10767795
; Publication No. US20040181830A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Cao, Yongwei
; APPLICANT: Zhou, Yihua
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53534)B
; CURRENT APPLICATION NUMBER: US/10/767, 795
; CURRENT FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 117596
; SEQ ID NO 1304
; LENGTH: 1047

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?      LENGTH: 986
?      TYPE: DNA
?      ORGANISM: Zea mays
?      FEATURE:
?      OTHER INFORMATION: clone ID: LIB3180-039-D5_F1
US-10-425-114-20345

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Alignment Scores:	
Pred. No.:	3,38e-99
Score:	863.50
Percent Similarity:	93.78
Best local Similarity:	82.904
Query Match:	86.428
DB:	7
Length:	986
Matches:	160
Conservative:	21
Mismatches:	11
Indels:	1
Gaps:	1

US-10-688-481-11 (1-192) x US-10-425-114-20345 (1-986)

QY	1	MetPheLeuValAspTyrPheTyrGlyPheLeuAlaSerIleGlyLeuTrpGlnGlyGlu	20
Db	130	ATGTTCTCTGGGACTGGTCTTACGGGGGCTGGCTCCCTCGGCTGTGGCAAGAGAG	189
QY	21	AlaIysIleLeuPheLeuGlyLeuAspAenAlaGlyLeuThrThrLeuLeuHisMetLeu	40
Db	190	GCGAAGATCTCTTCTCTCGGCTTCGACAAAGCCGGCAAGACACCGCTCTCCACATGCTC	249
QY	41	LysAspGlyuLysLeuGlyGlnHisGlnProThrGlnTyrProThrsertGluGluLeuSer	60
Db	250	AAGACGAGCGGGTTGGTGCAGACACAGCCGACGACACCCGACGTGGAGGAGCTCAGC	309
QY	61	IleAenATGValLysPheLysAlaPheAspLeuGlyGlyHisThrIleAlaArgATGVal	80
Db	310	ATCGCAAGATCAAGTCAAGGCTTCGACTCGGGGGCCACCAAGTGGCGCGCGCTGC	359
QY	81	TyrArgAspTyrTyrAlaLysValAspAlaIleValTyrLeuValAspAlaValAspArg	100
Db	370	TGGAAGGATTACTACGCAAAAGGTTGATGCTTGAAGTATACCTGGTAGATGGATGATGAAG	429
QY	101	GluArgPheAlaGluSerLysLysGlyLeuAspSerLeuLeuSerLysAspSerLeuSer	120
Db	430	GAGCATTATGCTGAATCAAAAAAGAGCTGAGCGCTCTCTGCAGATATATCTTTGGCA	489
QY	121	GluValProValLeuValLeuGlyLysValLysIleAspIleProTyrAlaSerSerGluAsp	140
Db	490	AATGTTCCATTTCTCATCTCTTGGACAAAGATTGAATATCCGATCTGCTCTTGAAAGG	549
QY	141	GluLeuArgPheThrLysGlyLeuThr---MetThrThrGlyLysGlyLysThrValAenLeu	159
Db	550	GAGCTGGCGGTATCACCCTAGCGCTTAGCACTTCACACCGGGAAGGCAAGTCAACCTT	609
QY	160	GlyAspSerAsnIleArgProIleGluValPheMetCysSerIleValArgLysMetGly	179
Db	610	GCGCAGTCCAAATGTCGGCGCACCTTGAGGTTTTCATGTGCAGTGTGTTGCGCAAGATGCGC	669
QY	180	TyrGlyGluGlyPheLysTrpMetThrGlnTyrIleLys	192
Db	670	TACGGCGAATGTTTCAAGTGGGCTCTCCCAATACATTAAG	708

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 9, 2005, 01:50:33 ; Search time 706 Seconds
(without alignments)
101.672 Million cell updates/sec

Title: US-10-688-481-11

Perfect score: 998
Sequence: 1 MFLVDMFYGFSLSIGLMQKE.....STVRKKYGEGRKMTQYIK 192

Scoring table:
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Xgapop 10.0 , Xgapext 0.5
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Searched: 3392430 seqs, 186927314 residues

Total number of hits satisfying chosen parameters: 6784860

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Database : Published Applications NA New:

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2: /cgn2_6/prodata/2/pubpna/US06_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	269.5	27.0	3891	US-10-955-054A-178	Sequence 178, App
2	248.5	24.9	2960	US-10-821-234-226	Sequence 226, App
3	221	22.1	591	US-11-093-746A-15	Sequence 15, App1
4	221	22.1	3791	US-11-093-746A-1	Sequence 1, App1
5	216.5	21.7	1650	US-10-821-234-76	Sequence 76, App1
6	167	16.7	824	US-10-750-185-37034	Sequence 37034, A
7	167	16.7	2946	US-10-750-185-27986	Sequence 27986, A
8	165.5	16.6	746	US-11-099-691-26	Sequence 26, App1

9	151.5	15.2	976	US-10-750-185-46137	Sequence 46137, A
10	130.5	13.1	676	US-10-750-185-28179	Sequence 28179, A
11	119.5	12.0	618	US-10-821-234-602	Sequence 602, App
12	99.5	10.0	2010	US-10-821-234-248	Sequence 248, App
13	97.5	9.8	1917	US-10-821-234-217	Sequence 217, App
14	90	9.0	2163	US-10-793-626-2057	Sequence 2057, App
15	90	9.0	3792	US-10-793-626-3396	Sequence 3396, App
16	89.5	9.0	1347	US-10-618-320A-27	Sequence 27, App
17	89.5	9.0	1353	US-10-618-320A-28	Sequence 28, App1
18	89.5	9.0	1377	US-10-618-320A-2	Sequence 2, App1
19	89	8.9	1365	US-11-112-944-3	Sequence 3, App1
20	89	8.9	2631	US-11-074-176-321	Sequence 321, App
21	89	8.9	2649	US-11-074-176-87	Sequence 87, App1
22	89	8.9	3128	US-10-821-234-831	Sequence 831, App
23	85.5	8.6	2005	US-10-821-234-531	Sequence 531, App
24	85	8.5	1185	US-10-821-234-774	Sequence 774, App
25	81.5	8.2	903	US-11-074-176-361	Sequence 361, App
26	81.5	8.2	924	US-11-074-176-253	Sequence 253, App
27	78.5	7.9	651	US-10-821-234-631	Sequence 631, App
28	78.5	7.9	1656	US-10-909-125-829	Sequence 829, App
29	78.5	7.9	134499	US-11-117-187-192	Sequence 192, App
30	76.5	7.7	1251	US-10-793-626-1461	Sequence 1461, App
31	76.5	7.7	3528	US-10-793-626-3791	Sequence 3791, App
32	76.5	7.7	171336	US-10-933-025-24	Sequence 24, App1
33	76	7.6	753	US-11-055-822-1025	Sequence 1025, App
34	76	7.6	1997	US-10-750-185-29682	Sequence 29682, A
35	75.5	7.6	1062	US-11-060-023-3	Sequence 3, App1
36	75.5	7.6	1062	US-11-060-023-5	Sequence 5, App1
37	75.5	7.6	1062	US-11-060-023-7	Sequence 7, App1
38	75.5	7.6	1080	US-11-060-023-1	Sequence 1, App1
39	75	7.5	2324	US-10-821-234-4	Sequence 4, App1
40	74.5	7.5	1128	US-11-060-023-9	Sequence 9, App1
41	74.5	7.5	3669	US-11-186-284-174	Sequence 174, App
42	73	7.3	582	US-10-821-234-587	Sequence 587, App
43	73	7.3	2829	US-10-467-657-5507	Sequence 5507, App
44	73	7.3	3288	US-10-467-657-5707	Sequence 5707, App
45	73	7.3	3337	US-10-793-626-3655	Sequence 3655, App

ALIGNMENTS

RESULT 1
US-10-955-054A-178
; Publication No. US20050266420A1
; GENERAL INFORMATION:
; APPLICANT: PUSZTAI, LAJOS
; APPLICANT: SYMMANS, W. FRASER
; APPLICANT: HESS, KENNETH R.
; APPLICANT: AVERS, MARK
; TITLE OF INVENTION: MULTIGENE PREDICTORS OF RESPONSE TO CHEMOTHERAPY
; FILE REFERENCE: VTXC:880US
; CURRENT APPLICATION NUMBER: US/10/955,054A
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 178
; LENGTH: 3891
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-955-054A-178

Alignment Scores:
Pred. No.: 2.76e-25
Score: 269.50
Percent Similarity: 53.18%
Best Local Similarity: 34.10%
Query Match: 27.00%
DB: 6
US-10-688-481-11 (1-192) x US-10-955-054A-178 (1-3891)

Length: 3891
Matches: 59
Conservative: 33
Mismatch: 70
Indels: 11
Gaps: 2

QY 19 LyGluAlaLysIleuPheLeuGlyLeuAspAsnAlaGlyLysThrThrLeuLeuHis 38
:::|||||
DB 204 CAGAGGTGAAGAAATCTTCTCTCGCTTGATATGCTGCAGACACACTCTTCTGAAG 263
QY 39 MetLeuLysAspGlyLysLeuGlyGlnHisGlnProThrGlnTyrProThrSerGluGlu 58
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DB 264 CAGCTTGCACTGGAAGACATGACCAATCACACCTTACAGGGTTTCAACATCAAAAGT 323
QY 59 LeuSerIleAsnArgValLysPheLysAlaPheAspLeuGlyGlnHisThrIleAlaArg 78
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DB 324 GTACAAATCAACAAGGTTTTAACTGAATGTATGGGACATTTGGTGACAGAGAAATCGA 383
QY 79 ArgValITPArgAspTyrTyrAlaLysValAspAlaIleValTyrLeuValAspAlaVal 98
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DB 384 CCATACCTGGAGAAATTTATTTGAAATACCGATATTTCTTATATATGTAATGACAGCGCA 443
QY 99 AspArgGluArgPheAlaGluSerLysLeuGlyLeuAspSerLeuLeuSerAspAspSer 118
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DB 444 GACGAAAAAAGATTTGAAGAGACCGGTCAGAACTTACGGCAATTTACGAGAGAAAGAAA 503
QY 119 LeuSerGlnValProValLeuValLeuGlyAsnLysIleAspIleProTyrAlaSerSer 138
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DB 504 CTAAGTTGTGTGCCAGTGTCTCATCTTGTCTAATAAGCAGATTTGCTCAGACAGCCCT 563
QY 139 GluAspGluLeuArgPheThrLeuGlyLeuThrMetThrThrGlyLysGlyThrValAsn 158
|||
DB 564 GCCTCTGAAATTT-----GCAGAGAGG---CTGAAAC 590
QY 159 LeuGlyAspSerAsnIleArgProIleGluValPheMetCysSerIleValArgLysMet 178
|||
DB 591 CTGCATACCATCCGCGACCGAGTCTGCGCATCCAGTCTTCTCAGCTCTCAGCAGAGAG 650
QY 179 GlyTyrGlyGlnGlyPheLysTyrPheThrGlnTyrIle 191
DB 651 GCGCTGAGATGGCATGACATGGGTCTGCAAAATATGC 689

RESULT 2

US-10-821-234-226
; Sequence 226, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarman, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: PC_SEQ_genes Version 1.0
; SEQ ID NO 226
; LENGTH: 2960
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-226

Alignment Scores:

Pred. No.: 1,29e-22 Length: 2960
Score: 248.50 Matches: 62
Percent Similarity: 47.94% Conservative: 31
Best Local Similarity: 31.96% Mismatches: 78
Query Match: 24.90% Indels: 23
DB: 6 Gaps: 4

US-10-688-481-11 (1-192) x US-10-821-234-226 (1-2960)

QY 3 LeuValAspTyrPheTyrGlyPheLeuAlaSerIleGlyLeuTyrGlnLysGluAlaLys 22
|||
DB 196 CTGCTGACACTGCTTCCTGCTC-----TTCTGGAAGAGAGATGAG 240

QY 23 IleuPheLeuGlyLeuAspAsnAlaGlyLysThrThrLeuLeuHisMetLeuLysAsp 42
:::|||||
DB 241 CTGACGCTCGTGGGCTGCGAGTACTCGGCAAGCCACTTGTCAATGTCATCGCTCA 300
QY 43 GlnLysLeuGlyGlnHisGlnProThrGlnTyrProThr-----SerGluGlu 58
|||
DB 301 -----GCTCAATTCAGTAAAGATATGATACCCACAGTGGGCTTCAACATGAGAG 351
QY 59 LeuSerIleAsnArgValLysPheLysAlaPheAspLeuGlyGlnHisThrIleAlaArg 78
:::|||||
DB 352 GTAACTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 411
QY 79 ArgValITPArgAspTyrTyrAlaLysValAspAlaIleValTyrLeuValAspAlaVal 98
:::|||||
DB 412 AGCATGTGGAGGCGGTATTCAGAGAGTAAATGCTTTTATTAATGATGATGATGCA 471
QY 99 AspArgGluArgPheAlaGluSerLysLeuGlyLeuAspSerLeuLeuSerAspAspSer 118
|||
DB 472 GATGTGAAAAAGTATGAAAGCTTCCGAAATGAGCTTACATATTTCTTAGATTAACACAG 531
QY 119 LeuSerGlnValProValLeuValLeuGlyAsnLysIleAspIleProTyrAlaSerSer 138
|||
DB 532 TTACAAGAAATTCAGTGTCTAGTCTTGAAACAGAGAGATCTTCTTAATGCTTGAT 591
QY 139 GluAspGluLeuArgPheThrLeuGlyLeuThrMetThrThrGlyLysGlyThrValAsn 158
|||
DB 592 GAGAAACAGCTA-----ATTGAAAAATGAAAT 618
QY 159 LeuGlyAspSerAsnIleArgProIleGluValPheMetCysSerIleValArgLysMet 178
|||
DB 619 CTGCTGCTATTACAGATTAAGAAATTTGCTCTATTCAATTTCTTGCAAGAAAGAGAT 678
QY 179 GlyTyrGlyGlnGlyPheLysTyrPheThrGlnTyrIle 192
DB 679 AATATAGATATCAACATCTGAGTCTTATTCAGATATCAAA 720

RESULT 3

US-11-093-746A-15
; Sequence 15, Application US/11093746A
; Publication No. US20050266443A1
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo M.
; APPLICANT: Calin, George A.
; TITLE OF INVENTION: NOVEL TUMOR SUPPRESSOR GENE AND
; FILE REFERENCE: 3589,1015-003
; CURRENT APPLICATION NUMBER: US/11/093,746A
; CURRENT FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: PCT/US2003/032270
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 60/417,842
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 591
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-093-746A-15

Alignment Scores:

Pred. No.: 6.3e-20 Length: 591
Score: 221.00 Matches: 54
Percent Similarity: 52.67% Conservative: 25
Best Local Similarity: 36.00% Mismatches: 57
Query Match: 22.14% Indels: 14
DB: 7 Gaps: 2

US-10-688-481-11 (1-192) x US-11-093-746A-15 (1-591)

QY 20 GluAlaLysIleLeuPheLeuGlyLeuAspAsnAlaGlyLysThrThrLeuLeuHisMet 39
|||
DB 34 GAAGCCAGGTGATGATGATGGCTGGACTCGGCGGCAAGACCAAGCTCTTACAG 93

Db 1127 AGATGACAGCATGCTGAAAAGATTTCAGAGATGACATGAGCTGCAGAAAATGCTTCT 1068
Qy 115 rAspAspSerLeuSerGlnValProValLeuValLeuGlyAsnLysIleAspIleProTy 135
Db 1067 GGATGATGAAATTTGAGAGATGACATGCTGCTACTTTTGCAAAACAAAGATTGGCCAAA 1008
Qy 135 rAlaSerSerGlnAspGluLeuAspGlnPheThrLeuGlyLeuThrThrThrGlyLysG1 155
Db 1007 TGCTATGAGCCATGATGAGTAAAGACAGATAAACTGAGGCTT----- 968
Qy 155 yThrValAsnLeuGlyAspSerAsnIleArgProIleGluValPheMetCysSerIleVal 175
Db 967 -----CAGTCTCTTCGTAACAGAAATGATGATGTTCAAGCCACTTG 927
Qy 175 lArgLysMetGlyTyTrGly-----GluGlyPheLysTrpMetThr 188
Db 926 TGCAACACAAAGAACTGGTCTGTATGAAAGACTTGACTGGCTGTCA 881

RESULT 6
US-10-750-185-37034/c
Sequence 37034, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM11100-2
CURRENT APPLICATION NUMBER: US/10/750,185
PRIOR FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIn version 3.1
SEQ ID NO 37034
LENGTH: 824
TYPE: DNA
ORGANISM: Bovine 19866880402345
US-10-750-185-37034

Alignment Scores:
Pred. No.: 2,17e-12 Length: 824
Score: 167.00 Matches: 43
Percent Similarity: 50.00% Conservative: 23
Best Local Similarity: 32.58% Mismatches: 50
Query Match: 16.73% Indels: 16
Gaps: 4

US-10-688-481-11 (1-192) x US-10-750-185-37034 (1-824)

Qy 64 ValLysPheLysAlaPheAspLeuGlyGlyHisThrIleAlaArgArgValTrpArgAsp 83
Db 786 GTCCTGCTCAGCGTCTGGAGCTTGAGACAGAAAGATGAGCCACCTGGGGCTC 727
Qy 84 TyrTrpAlaLysValAspAlaIleValTyrLeuValAspAlaValAspArgGluArgPhe 103
Db 726 TACTGTGAGAACTGATGAGCTGATGATGTTGGACATGACAGACACACCGACTT 667
Qy 104 AlaGluSerLysGluLeuAspSerLeuSerLeuSerAspAspSerLeuSerGlnValPro 123
Db 666 GAAGACTCCAGAAAGAGTTTGACACATCTTGAAGATGATGATTTAAAAAGTGGCT 607
Qy 124 ValLeuValLeuGlyAsnLysIleAspIleProTyrAla---SerSerGluAspGluLeu 142
Db 606 GTGCTCTGTTAGCCAAACAAAGATATGCTGAGCTTAAAGTCCGAGACATACACC 547
Qy 143 ArgPheThrLeuGlyLeuThrMetThrThrGlyLysGlyThrValAsnLeuGlyAspSer 162
Db 546 AGAGTGTTC-----AAAGTGAAGCAACTCTGACGTGACCGG 511

Qy 163 Asn-----IleArgProIleGluValPheMetCysSerIleValArgLysMetGlyTyr 180
Db 510 AACTGTGCTGTCGAGCC-----TGCTGTCCGCTCACTGGGAGACGGGCTA 466
Qy 181 GlyGluGlyPheLysTrpMetThrGlnTyrIleLys 192
Db 465 ATGAGGGGTTCCAGAAATTAACTGATTTGTGAAA 430

RESULT 7
US-10-750-185-27986/c
Sequence 27986, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM11100-2
CURRENT APPLICATION NUMBER: US/10/750,185
PRIOR FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIn version 3.1
SEQ ID NO 27986
LENGTH: 2946
TYPE: DNA
ORGANISM: Bovine 19866880857076
US-10-750-185-27986

Alignment Scores:
Pred. No.: 1.44e-11 Length: 2946
Score: 167.00 Matches: 30
Percent Similarity: 86.67% Conservative: 9
Best Local Similarity: 66.67% Mismatches: 6
Query Match: 16.73% Indels: 0
Gaps: 0

US-10-688-481-11 (1-192) x US-10-750-185-27986 (1-2946)

Qy 14 lIleGlyLeuTrpGlnLysGluAlaLysIleLeuPheLeuGlyLeuAspAsnAlaGlyLys 33
Db 147 TTAGGACTCTACACAGAAATCTGAAAATCTGTATCTTGCGTTTGACATGACGGCAA 88
Qy 34 ThrThrLeuLeuHisMetLeuLysAspGluLysLeuGlyGlnHisGlnProThrGlnTyr 53
Db 87 ACCACTCTTACACATGCTCAAGATGACAGACTGGGCGAGCATGTTCCAACTTACAT 28
Qy 54 ProThrSerGluLys 58
Db 27 CCAAGTAGGTTTGA 13

RESULT 8
US-11-099-691-26
Sequence 26, Application US/11099691
Publication No. US20050260644A1
GENERAL INFORMATION:
APPLICANT: INCYTE PHARMACEUTICALS, INC.
APPLICANT: BANDMAN, Olga
APPLICANT: HITLMAN, Jennifer L.
APPLICANT: LAL, Preeti
APPLICANT: YUE, Henry
APPLICANT: TANG, Y. Tom
APPLICANT: PATTERSON, Chandra
APPLICANT: BAUGHN, Mariah R.
APPLICANT: YANG, Junming
TITLE OF INVENTION: CELL SIGNALING PROTEINS
FILE REFERENCE: PF-0521 PCT

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; CURRENT APPLICATION NUMBER: US/11/099,691
; CURRENT FILING DATE: 2005-04-06
; PRIOR APPLICATION NUMBER: US/09/700,444
; PRIOR FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 60/085,343
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/098,010
; PRIOR FILING DATE: 1998-08-26
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PERL Program
; SEQ ID NO: 26
; LENGTH: 746
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; OTHER INFORMATION: Incyte Clone 3315936
; US-11-099-691-26

Alignment Scores:
Pred. No.: 2,998-12 Length: 746
Score: 165.50 Matches: 41
Percent Similarity: 54.48% Conservative: 31
Best Local Similarity: 31.34% Mismatches: 56
Query Match: 16.58% Indels: 5
DB: 7 Gaps: 3

US-10-688-481-11 (1-192) x US-11-099-691-26 (1-746)
Qy 18 GlnlyGlnlyAlaLysIleLeuPheLeuGlyLeuAspAsnAlaGlyLysThrThrLeuLeu 37
Db 115 GAGAAAACAGACAAATCTAGTGTCTGGCTGGATGAGCAGGAAACAGATGCTCTG 174
Qy 38 HiMetLeuLysAspGlyLysLeuGlyGlnHisGln-----ProThrGlnTrpProThr 55
Db 175 CACTCTTACTGCTCAACAGAGATC---CAGCAGATGTGGCACCACCCAGGTTTCCAT 231
Qy 56 SerGlnLysLeuSerIleAsnArgValLysPheLysAlaPheAspLeuGlyLysThr 75
Db 232 GCAGTTTGACCTCAACACTGAGACAGCCAGATGAGTCTCGAGATGTGTGCAGTAA 291
Qy 76 IleAlaArgArgValTrpArgAspTrpTrpAlaLysValAspAlaIleValTrpLeuVal 95
Db 292 CCTTTTCGCTCTACTGGAATGTACTTCAAGGATTTGCTGCTGATCTTGTGTG 351
Qy 96 AspAlaValAspArgLysArgPheAlaGlySerLysLysGlnLeuAspSerLeuLeuSer 115
Db 352 GATTCAAGACATCAACAGCCGATTACTGAGCCAGAAATACCTTCATCAGTAATTGCA 411
Qy 116 AspAspSerLeuSerGlnValProValLeuValLeuGlyLysLeuValIleProTrp 135
Db 412 GCAAAACCCAGTA-----CTTCTCTGTGGTTGTTCACAAACAAACAGATCTTGAAGA 465
Qy 136 AlaSerSerGlnAspGlnLeuArgPheThrLeuGlyLeuThr 149
Db 466 GCCTATCACTATCAGATATCATGAGGCTTTGGCATTAATCT 507

RESULT 9
US-10-750-185-46137
; Sequence 46137, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM11100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
```

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; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 46137
; LENGTH: 976
; TYPE: DNA
; ORGANISM: Bovine
; US-10-750-185-46137

Alignment Scores:
Pred. No.: 3,528-10 Length: 976
Score: 151.50 Matches: 39
Percent Similarity: 46.88% Conservative: 21
Best Local Similarity: 30.47% Mismatches: 27
Query Match: 15.18% Indels: 41
DB: 6 Gaps: 4

US-10-688-481-11 (1-192) x US-10-750-185-46137 (1-976)
Qy 27 GlyLeuAspAsnAlaGlyLysThrThrLeuHisMetLeuLysAspGlu----- 43
Db 609 GGCCTGACAAATGCGGCAAGACATCTCAAGAGATTCAACCGTGAAGACATCGAC 668
Qy 44 -----LysLeuGly--GlnHisGln----- 49
Db 669 ACCATCTCCCACTGGGCTTCAACATCAAGACTTGAGACCGAGGTAAGCGGG 728
Qy 50 -----ProThrGlnTrp----- 53
Db 729 TCCCCGAGGCGCGCTGCGCCAGCAGGAGGCGGCGGCGGCGGACTGACC 788
Qy 54 -----ProThrSerGlnLysLeuSerIleAsnArgValLysPheLysAlaPheAsp 71
Db 789 CTGACAGCCCTCACT-----GCCCTGTCCAGATTCAAGCTGAACATTGGAGT 836
Qy 71 euGlyGlyHisThrIleAlaArgArgValTrpArgAspTrpTrpAlaLysValAspAla 91
Db 837 TGGGCGGCAAGAGTCCCTGCGGTCTTACTGCGGAACTTGTGAGACCGAGCGCC 896
Qy 91 leValTrpLeuValAspAlaValAspArgLysArgPheAlaGlySerLysLysGlnLeu 111
Db 897 TCATCTGGGTGGTGGACAGCGCCGACCGCAGCGCATGACGACTGCGAGCGGAGCTCC 956
Qy 111 spSerLeuLeuSerAspAsp 117
Db 957 AGAACCTGTGTGTGAGAG 976

RESULT 10
US-10-750-185-28179
; Sequence 28179, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM11100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 28179
; LENGTH: 676
; TYPE: DNA
; ORGANISM: Bovine
; US-10-750-185-28179 19866880693146
```

Alignment Scores:	
Pred. No.:	1.44e-07
Score:	130.50
Percent Similarity:	56.18%
Best Local Similarity:	35.96%
Query Match:	13.08%
DB:	6
Length:	676
Matches:	32
Conservative:	18
Mismatches:	37
Indels:	1
Gaps:	1

US-10-688-481-11 (1-192) x US-10-750-185-28179 (1-676)

QY 20 GlnAlaValLeuLeuPheLeuGlyLeuAspAspAlaGlyLeuThrThrLeuLeuMet 39
 Db 405 GAAACCCAGGGGGATGATGATGAGCCCTGAGACTGGCCGGCAAGACCAACCTCTGTACAA 464
 QY 40 LeuLysaApGluLysLeuGlyGlnHISglnProThrGlnTyProThrSerGluGluLeu 59
 Db 465 CTGAAGGGACCAACGAGCTGTGGACACCCCTGCCACCGTGGGTTCACAGTGGAGCCCTTC 524
 QY 60 SerLe---AsnArgValLysPheLysValaPheAspLeuGlyGlnHISThrIleAlaArg 78
 Db 525 GAGGCCCCCGGACAGCGCTGCCTCACCTCTGGAGATGTGGGGGGACAGGCCACTCAGG 584
 QY 79 ArgValTrrArgAspTyrTyralysValaAspAlaIleValTyrlLeuValAspAlaVal 98
 Db 585 GCCAGCTGGAAGAGACTACCTGGAGGGGCAAGCGCGCTCTGTGTTTGTCTGTGACAGCA 644
 QY 99 Asp-ArgGluArgPheAlaGluSer 106
 Db 645 GACGAGGAGCCCGCTTGGCCGAGGCA 669

RESULT 11
US-10-821-234-602

Alignment Scores:	
Pred. No.:	3.9e-06
Score:	119.50
Percent Similarity:	40.53%
Best Local Similarity:	25.26%
Query Match:	11.97%
DA:	6
Length:	618
Matches:	48
Conservative:	29
Mismatches:	60
Indels:	11
Gaps:	10

US-10-688-481-11 (1-192) X US-10-821-234-602 (1-618)

QY 22 LysIleLeuPheLeuGlyLeuAspAsnAlaGlyIleThrThreLeuLeuHisMetLeuLys 41
 QY 37 AGGTTACTTTCGATTGGCGACTCAGGGGTGGAAAGCTTCGCTTCTTCTTAGCTTGA 96
 QY 42 AspGluLysLeuGlyGlnHisGlnProThrGlnTyProThrSerGluLeuSerIle 61
 QY 97 GATGAT-----ACATATACAGAAAGCTTACTTC 122
 QY 62 AsnArgVal-----LysPheLysAlaPheAspLeuGlyGlyHisThrIleAla 77

[illegible]

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RESULT 12
US-10-821-234-248
; Sequence 248, Application US/10621234
; Publication No. US2005025511A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andermann, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_genes Version 1.0
; SEQ ID NO 248
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-248

```

Alignment Scores:	
Pred. No.:	0.016
Score:	99.50
Percent Similarity:	42.73%
Best Local Similarity:	28.18%
Query Match:	9.97%
DB:	6
Length:	2010
Matches:	31
Conservative:	16
Mismatches:	38
Indels:	25
Gaps:	3

US-10-688-481-11 (1-192) x US-10-821-234-248 (1-2010)

[illegible]

```
Db 773 CACGGCTGTGAGCGAAGAGTGCATCTTGAGGGCGCTCAAGCATCATCTTC 832
Qy 94 -----leuValAspAlaValAspArgIu-----ArgPhe 103
Db 833 TGGCTAGCCTTGAGCGCGCTATGACTGTGCTAGCGAGACAGAGATGAACCGCAG 892
Qy 104 AlaGluSerIysIysGluLeuAspSerLeuLeuSerAspAspSerLeuSerGluValPro 123
Db 893 CAGGAGAGCATGAAGCATTCGATAGCATCTGCACAACAAGTGTTCACAGACAGCTCC 952
Qy 124 ValIeuValIeuGluIysIysIleAspIle 133
Db 953 ATCATCTCTTCTCTCAACAGAGAGACCTG 982

RESULT 13
US-10-821-234-217
; Sequence 217, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmant, Susan
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: PL_SEQ_genes Version 1.0
; SEQ ID NO 217
; LENGTH: 1917
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-217

Alignment Scores:
Pred. No.: 0.0202 Length: 1917
Score: 97.50 Matches: 45
Percent Similarity: 38.71% Conservative: 27
Best Local Similarity: 24.19% Mismatches: 70
Query Match: 9.77% Indels: 45
DB: 6 Gaps: 7

US-10-688-481-11 (1-192) x US-10-821-234-217 (1-1917)
Qy 22 LysIleuPheLeuGluIysLeuAspAsnAlaGlyIysThrThrLeuLeuHisMetLeuLys 41
Db 75 AAGCTGCTTTGATGTGGCGACTCAGGCGTGGCGAAGTCAGCTGCTCTCGCGTTGCT 134
Qy 42 AspGluIysLeuGluIysGlnHisGlnProThrGlnTyrProThrSerGluIleuSerIle 61
Db 135 GATGAC-----ACGTACACAGAGAGCTACATC 161
Qy 62 AsnArgVal-----LysPheLysAlaPheAspLeuGluIysIleThrIleAla 77
Db 162 AGCAGCATCGGGGTGACCTTCAAGATCCGAACCATCGAGCTGATGGCAAAACTATCAAA 221
Qy 78 ArgArgValTrp-----ArgAspTyrTyr 85
Db 222 CTTCAGATCTGGACACAGCGGCGCAAGACGGTTCGGACATCACTTCCAGCTACTAC 281
Qy 86 AlaLysValAspAlaIleValTyrLeuValAspAlaValAspArgIuArgPheAlaGlu 105
Db 282 CGGGGGGCTCATGGCATCATCGTGTATGACGTCACTGACAGAAATCTTAAGCAAC 341
Qy 106 SerIysLysGluLeuAspSerLeuLeuSerAspAspSerLeuSerGluValProValIleu 125
Db 342 GTGAAGCAAGTGTGCTGACGAGGAGATGACCGCTAT-GCCAGCGAGAACGTCAATAAGCTC 400
Qy 126 ValIeuGluIysIleAspIleProTyrAlaSerSerGluAsp----- 140
```

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Db 401 CTGTGGGCAACAAGAGCACTCACACCAAGAAAGTGTGGACAACAACAGCGCAAG 460
Qy 141 GluLeuAspPheThrIleuGluIysThrMet-----ThrThrIysGluIysThrValAsn 158
Db 461 GAGTTTGACAGACTCTTGTGGCATCCCTCTTGGAGACAGCGCCAAAGAAATGCCACCAAT 520
Qy 159 IeuGluAspSerAsnIleArgProIleGluValPheMet-----CysSerIleVal 175
Db 521 GTCGAG-----CAGGCTTATATACATGAGCTGTGAAATCAAA 559
Qy 176 ArgLysMetGlyTyrGly 181
Db 560 AAGCGATGGGCGCTGGA 577

RESULT 14
US-10-793-626-2057
; Sequence 2057, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMBERLY WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P03480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2057
; LENGTH: 2163
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-2057

Alignment Scores:
Pred. No.: 0.251 Length: 2163
Score: 90.00 Matches: 33
Percent Similarity: 48.00% Conservative: 27
Best Local Similarity: 26.40% Mismatches: 57
Query Match: 9.02% Indels: 8
DB: 6 Gaps: 3

US-10-688-481-11 (1-192) x US-10-793-626-2057 (1-2163)
Qy 18 GlnLysGluAlaLysIleLeuPheLeuGluIysLeuAspAsnAlaGlyIysThrThrLeuLys 37
Db 664 GAACTGCAGCAAGTTGTATACATCATGGGCGACAGTACCATGTAACGACTTTATTA 723
Qy 38 HisMetLeuLysAspGluIysLeuGluIysGlnHisGlnPro-----ThrGlnTyrPro 54
Db 724 GATTCTATTGCTAACTAAAGTTACAGAAAGAGAGAGTGGCGGAATCACTCAACATATT 783
Qy 55 ThrSerGluGluLeuSerIleAsnArgValLysPheLysAlaPheAspLeuGluIysHis 74
Db 784 GGTGCTTATCAATTAAGAAATTACAGGTAAATAATTACCTCTTATCATCTCTCGACAT 843
Qy 75 ThrIleAlaArgArgValTrpArgAspTyrTyrAlaLysValAspAlaIleValTyrLeu 94
Db 844 GCT--GCAATTACGACTATGCTGCAAGTGTCTCAAGTTAAGTTATTTACAAATTTTA 900
Qy 95 ValAspAlaValAspArgIuArgPheAlaGluSerIysLysGluLeuAspSerLeuLys 114
Db 901 GTGTGGCGCGCATGATGATGTGTGATGCTCAAAACAATTGAAGCTTAATATACGCTAAA 960
Qy 115 SerAspAspSerLeuSerGlnValProValIleuValIeuGluIysIleAspIlePro 134
Db 961 GAA-----GCAGAAATCACTGACGATTTGTGACGTAAACAAATGTGATTAACCA 1008
Qy 135 TyrAlaSerSerGlu 139
```

Db 1009 ACTGCTAACCTGAT 1023

RESULT 15

US-10-793-626-3396/c
; Sequence 3396, Application US/107933626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUI480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3396
; LENGTH: 3792
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-3396

Alignment Scores:

Pred. No.:	0.578	Length:	3792
Score:	90.00	Matches:	33
Percent Similarity:	48.00%	Conservative:	27
Best Local Similarity:	26.40%	Mismatches:	57
Query Match:	9.02%	Indels:	8
DB:	6	Gaps:	3

US-10-688-481-11 (1-192) x US-10-793-626-3396 (1-3792)

QY 18 GlnlyseglualylylleuPhelengllyleuAspAenlaaglylysthrThreuleu 37
Db 3290 GAACGTCGACGATTGATACATCATGCGCCACGTCAGCATGTTAAACGACTTTATTA 3231
QY 38 Histetleuysaepglulyleuclglylnhislnpro-----ThrglnTyPro 54
Db 3230 GATTCTATTCGTAACTAACTTACAGAGAGAGCTGGCGGAATCATCAACATATT 3171
QY 55 ThrserugiuleuserilleAsnaryValysPheylsAlaPheAspLeuglylyHis 74
Db 3170 GGTGCTTATCAATTGAATAATTCAGCTAAATAATTCGTTCTTAGATACCTCGACAT 3111
QY 75 ThrillealargargValTrrpArgAspTyTyralyValAspAlaIleValTyrlou 94
Db 3110 GCT---GCATTTACGACTATGCGTGCACGTGCTCAAGTTACTGATATTACAATTTTA 3054
QY 95 ValAspAlaValAspArgGluArgPheAlaGluSerlyslsGluLeuAspSerleuleu 114
Db 3053 GTCTGGCGCGTGAAGATGCTGATGCTCAACAAATTGAAGCTATTAAATCAACGCTAAA 2994
QY 115 SerAspAspSerleuserGlnValProValIleuValLeuGlyAsnlyslleAspIlePro 134
Db 2993 GAA-----GCAAGAACTACTTACGATTGTTGCACTAAACAAATTTGATTAACCA 2946
QY 135 TyralAspSerGlu 139
Db 2945 ACTGCTAACCTGAT 2931

Search completed: December 9, 2005, 04:18:09
Job time : 711 secs